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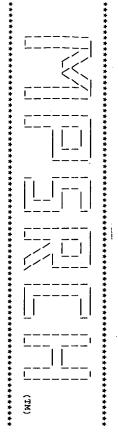
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

abular output not generated. p on: Tue Apr 20 13:57:56 1999; MasPar time 4.85 Seconds 174.525 Million cell updates/sec

Description: Perfect Score: Title: >US-08-836-455-2 (50-66) from US08836455.pep (2 of 3)

Scoring table: PAM 150 Gap 11 Sequence:

1 GINLHWLQQEPDGTIKR 17

Searched: 165420 segs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_bhage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 27.617; Variance 43.342; scale 0.637

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	ر ن	4	ω	2		Result
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-	- 1	SIGMA 3.	OUTER-CAPSID PROTEIN S	SIGMA 3.	SIGMA 3.	OUTER-CAPSID PROTEIN S	PROTEIN	OUTER-CAPSID PROTEIN S	יסי	HEMAGGLUTININ PRECURSO	CARNITINE RACEMASE HOM	PUTATIVE INDOLE-3-ACET	SIGMA 3.	TRANSPOSASE IS91.	Description						
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61	61	62	62	62	62	62	63	63	63	63	63	63	63	63	63	63	63	63	63	65	65	65	66	66
46.6	46.6	47.3	47.3	47.3	47.3	47.3	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	49.6	49.6	49.6	50.4	50.4
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RESULT 2 ID 086302 PRELIMINARY; PRT; 365 AA. AC 086302; DT 01-NOV-1996 (TREMBLREL. 01, CREATED) DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE) DE SIGMA 3. GN S4. OS REOVIRUS.	LNWLEKQPEGSVR 28	Query Match 55.7%; Score 73; DB 2; Length 426; Best Local Similarity 38.5%; Pred. No. 6.71e-02; Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps	RP SEQUENCE FROM N.A. RX MEDLINE; 92335017. RA MENDICLA M.V., DE LA CRUZ F.; RL NUCLEIC ACIDS RES. 20:3521-3521(1992). DR EMBL; X17114; G41842; KW PLASMID. SQ SEQUENCE 426 AA; 49982 MW; 226BE3E5 CRC32;	 OS ESCHERICHIA COLI. OS ESCHERICHIA COLI. OG PLASMID PSU2911. OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE. EN [1]	Ins
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SEQUENCE FROM N.A.
STRAIN-SEROTYPE 3;
MEDLINE; 95074914.
KEDL R.; SCHMECHEL S.C., SCHI
J. VIROL. 69:552-559(1995)
EMBL; U15083; G706880; ---
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J. VIROL. 69:552-559(1995).
EMBL: U15082; G706878; -.
SEQUENCE 365 AA; 41123 M
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VIRIDAE; 1
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Q86293;
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KEDL R., SCHMECHEL S.C., SCI
VIROL 69:552-559(1995).

MBL, U15074; G706862; -
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Local Similarity 40.0%;
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    INLHWLQQEPDGTIK 65
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Pred. No. 3
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                                        Score 69; DB 14;
Pred. No. 3.47e-01;
7; Mismatches 2
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MEDLINE; 95074914.
KEDL R., SCHMECHEL S.C., SCHI
J. VIROL. 69:552-559(1995).
EMBL; U15078; G706870; -.
SEQUENCE 365 AA; 41018 MW;
SEQUENCE FROM N.A.
STRAIN-SEROTYPE 3;
MEDLINE; 95074914.
KEDL R., SCHMECHEL 8
                                                                                    Q86299;
Q86299;
Q1-NOV-1996
Q1-NOV-1996
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Q86294;
01-NOV-1996
01-NOV-1996
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                                                        REOVIRUS
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MEDLINE; 95074914.
                                              VIRIDAE;
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VIRIDAE; DS-RNA
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VIRIDAE; DS-RNA NONENVELOPED
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
PUTATIVE INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE.
T27E13.12.
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01-NOV-1996
01-NOV-1996
01-NOV-1996
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KEDL R., SCHMECHEL S.C., SCR
VIROL, 69:552-559(1995).
                                                                                                                             STRAIN-CV. COLUMBIA;
ROUNSIEY S.D., LIN X., KETCHUM K.A., CROSB
SYKES S.M., KADL S., MASON T.M., KERLAVAGE
SOMERVILLE C.R., VENTER J.C.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ
EMBL, AC004165; G3150406; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. VIROL. 69:552-559(1995).
EMBL; U15080; G706874; -.
SEQUENCE 365 AA; 41074 M
                                                                                                                                                                                                                       ARABIDOPSIS THALIANA (MOUSE-EAR CRESS) EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOS
                                                                                                                                                                                                              CAPPARALES; CRUCIFERAE.
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51 INLHWLQQEPDGTIK 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHIFF L.A.;
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Pred. No. 7; Mismai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred.
7; M
                                                                Score 68; DB 10;
Pred. No. 5:19e-01;
8; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIRUSES; REOVIRIDAE; REOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                               58C38B31 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0B2EE93D CRC32;
                                                                                                           7C1FB50D CRC32;
                                                                                                                                                                                                                       ANGIOSPERMAE; DICOTYLEDONEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e 69; DB 14; L. No. 3.47e-01; Mismatches 2;
                                                                                                                                                            KERLAVAGE A.R.,
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 2;
                                                                                                                                                                                                                                                                                                        455
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                                                                                                                                                                                                                                                                                                                                                                                                           DB 14;
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                                                                                     Length 455
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                                                                                                                                                             ADAMS M.D.,
                                                                    Indels
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RESULT 12
ID Q98642
AC Q98642;
DT 01-FEB-1997
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Best Local :
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Best Local
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O23300; PRELIMINARY: DT., CREATED)
O1-JAN-1998 (TREMBLREL O5, LAST SEQUENCY
O1-AUG-1998 (TREMBLREL O7, LAST ANNOTAT
O1-AUG-1998 (TREMBLREL O7, LAST ANNOTAT
CARNITINE RACEMASE HOMOLOG.
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q82515
Q82515;
01-NOV-1996
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CHAIN
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU ARABIDOPSIS SEQUENCING PROJECT, ESSA;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ
EMBL, 297936; E327452; -
PFAM; PF00378; ECH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BEVAN M., STIEKEMA W., MURPHY G., WAMBUTT R., POHL T., TERR KREIS M., KAVANAGH T., ENTIAN K.D., RIEGER M., JAMES R., PUIGDOMENCH P., HATZOPOULOS P., OBERMAIER B., DUESTERHOFT JONES J., PALME K., ANSORGE W., DELSENY M., BANCROFT I., MESCHUELLER C., CHALWATZIS N.;
                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROHM C., HORIMOTO T., KAWAOKA
VIROLOGY 209:664-670(1995).
EMBL; U20466; G902767; -.
PFAM; PF00509; Hemagglutinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=A/TURKEY/MINNESOTA/1237/80 (H7N3);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFLUENZA A VIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEMAGGLUTININ PRECURSOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAPPARALES; CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95297170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /IRIDAE;
                                                                                                                                                                     239 IDFHWLLLDPNDTV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
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Similarity 47.1%;
                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                               6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 (TREMBLREL. ()
5 (TREMBLREL. ()
                                                                                                                                                                                                                                                                                                    356 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 AA;
  (TREMBLREL.
                                          PRELIMINARY;
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                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                      50.4%;
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                                                                                                                                                                                                                                                                                                    38596 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAWAOKA Y.,
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01, LAST SEQUENCE UPDATE)
06, LAST ANNOTATION UPDATE)
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Pred. No. 1.:
5; Mismatcl
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Pred. No.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE
  CREATED)
                                                                                                                                                                                                                                                                                                                                               HEMAGGLUTININ 2 CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
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                                                                                                                                                                                                                                                                                                    4C593717 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUSS J.,
                                          365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
1.15e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238
                                                                                                                                                                                                                                      DB 14;
1.15e+00;
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                                                                                                                                                                                                                                                          Length 356;
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                                                                                                                                                                                                               Indels
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Query Match
Best Local Similarity
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-L/C;
STRAIN-L/C;
STRAIN-L/C;
WETZEL J.D., WILSON G.J., BAEK w....
TANG D.S., DERMODY T.S.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA
EMBL; U63307; G1518828; ...
PONIENCE 365 AA; 41032 MW; 3F472E32 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q98639
Q98639;
Q1-FEB-1997
Q1-FEB-1997
Q1-AUG-1998
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01-FEB-1997
01-AUG-1998
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01-AUG-1998 (
OUTER-CAPSID
                                                                                        SEQUENCE FROM N.A.
STRAIN-PIIA1;
STRAIN-PIIA1;
WHIZEL J.D., WILSON G.J., BAER G.S., DUNNI
TANG D.S., DERMODY T.S.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ
EMBL; U63306; G1518826; -
SEQUENCE 365 AA; 41061 MW; IAELACD8 CR
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WETZEL J.D., WILSON G.J., BAER G.S., DUNNIGAN I TANG D.S., DERMODY T.S.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA EMBL; U63309; G1518832; -.
SEQUENCE 365 AA; 40989 MW; 5B158A9C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               OUTER-CAPSID
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VIRIDAE; DS-RNA NONENVELOPED
[1]
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VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE;
[1]
                                                                                                                                                                                                                                                                                                                                                   VIRIDAE; DS-RNA NONENVELOPED VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                               REOVIRUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INLHWLQQEPDGTIK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 (TREMBLREL. 02,
7 (TREMBLREL. 02,
8 (TREMBLREL. 07,
ID PROTEIN SIGMA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 (TREMBLREL. 02,
8 (TREMBLREL. 07,
ID PROTEIN SIGMA)
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7 (TREMBLREL. 02,
3 (TREMBLREL. 07,
1D PROTEIN SIGMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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   50.4%;
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02, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
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02, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
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07, LAST
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Score 66; DB 14;
Pred. No. 1.15e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 66; DB 14; L
Pred. No. 1.15e+00;
8; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 66; DB 14;
Pred. No. 1.15e+00;
8; Mismatches 2
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RESULT 15
ID 098641;
AC 098641;
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DF 00TER-CAPSID
GN S4.
OS RECVIRUS.
OS RECVIRUS.
OC VIRIDAE; DS-F
RN [1]
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RN TANG D.S., DE
RL SUBMITTED (JU
DR EMBL; U633088
SQ SEQUENCE 36
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SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA EMBL; U63308; G1518830; -...
SEQUENCE 365 AA; 41080 MW; D4C19A6F CRC32;
                                                                                                                                                                                                                                              OUTER-CAPSID
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                        129 VELNWLQVDPNSMFR
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                                                Local Similarity 33.3% ues 5; Conservative
51 INLHWLQQEPDGTIK 65
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7 (TREMBLREL. 02, I
8 (TREMBLREL. 07, I
ID PROTEIN SIGMA 3
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Pred. No.
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Search completed: Tue Apr 20 13:58:25 1999 Job time: 29 secs.

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Bovine P58 protein.	Human H11-scFv constr	Human Hil-scFv constr	NANUC-2 light chain,	nal	۳	Human vkappa65.8 frag	Ġ	vkappa65.3	ised anti-CI	light	chai	PB1.3/Humanised light	74	Ł	SQ.	PB1.3/Humanised light	CY1748RLB VL region.	D	Homologous sequences	bir	Protein able to bind	ht chain va	IL-2 chimeric antibod	2 chimeric anti	Murine anti-human cla	Anti-IL2R alpha antib	
.63e+0	.63e+0	.63e+0	1.63e+02	.63€	.63e+0	.63e+0	.63e+0	1.63e+02	.63e+0	.63e+0	1.63e+02	1.34e+02	. 34e	1.34e+02	•	1.34e+02	•	٠	•	:.	11		9.17e+01	.17e+0	•	9.17e+01	

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W09722699-A2.
26-JUN-1997.
19-DEC-1996; U20757.
13-DEC-1996; US-575762.
20-DEC-1996; US-575762.
26-JAN-1996; US-591965.
(KENT) UNIV KENTUCKY.
Chatterjee M, Chatterjee S
                                                                                                                                                                                                                                                                                                        Mus musculus.
Key
Peptide
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477119 standard; Protein; 145 AA.
W27119;
W27119;
04-JAN-1998 (first entry)
Murine monoclonal anti-idiotype antibody 11D10 VL region.
Monoclonal antibody 11D10; anti-idiotype antibody; mucin;
human milk fat globule; HMFG; tumour; breast cancer; vaccine.
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                                                                         /label FR3
/note "framework region 3"
109.117
/label CDR3
/note "complementarity determining region
1.127
/label FR1
/note "framework region 4"
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/note- "complementarity determining region
77..108
                                                                                                                                                                                 /label= FR2
/note= "framework region
70..76
                                                                                                                                                                                                                                                                                        /label= Sig_peptide
21..145
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/note= "complementarity determining region
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/note- "framework region 1"
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Prespecially breast cancer

SC Claim 9; Page 94; 130pp; English.

C This polypeptide sequence comprises the light chain variable region

C (VL) of monoclonal anti-idiotype antibody 11D10 produced by

hybridoma cell line ATC 12020. 11D10 was obtained by immunising

C naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype

C response. It elicits an immune response against a specific epitope

C induces an immunological response to HMFG in mice, rabbits, monkeys

C and patients with advanced HMFG-associated tumours. Pharmaceutical

and/or 11D10 polynucleotides (see also T85149-50) are claimed.

C and/or 11D10 polynucleotides (see also T85149-50) are claimed.

C polypeptides and/or 11D10 polynucleotides, including methods of

treating HMFG-associated tumours. 1D10 is also used in a claimed

detect or quantify anti-HMFG antibody.
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Best Local s
Matches
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30-MAR-1994; U03420.
30-MAR-1994; WO-U03420.
(IGEN-) IGEN INC.
Chiswell D, Darsley MJ, F
Martin MT, McCafferty J, S
Production of catalytic antibodies displayed on phage - by generating a gene library of antibody-derived domains and expressing ferrating a gene library of antibody-derived domains and expressing it in phage vectors

Disclosure; Fig 9; 133pp; English.

T04625 encodes R80078 mouse derived light chain RT3 phage antibody. The DNA was used in the prepn. of catalytic antibody (CA) producing bacteriophage. The CAs can be used to activate/deactivate a biological function in an animal by enhancing the rate of cleavage,
                                                                                                                                                                                                                                                        N-PSDB; T04625
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Mouse derived light chain RT3 phage antibody pattern A.
Light chain; RT3; murine; catalytic antibody; bacteriophage;
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R80078;
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N-PSDB; T85149.
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Local Similarity 100.0%;
Local Similarity 100.0%;
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48..78
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27..40
/note=
41..47
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N-terminal fragment"
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                                                                                                                                                                                                                                                                                                 Fitzgerald K, . Kenten Smith RG, Titmas RC,
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No. 1.06e+01;
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Claim 23; Page 70; 106pp; English.

CC Hybridoma antibodies have been produced with the spleen cells of CC BALB/c mouse that had received multiple injections of mercuric ions CC covalent compound which was covalently bound to keyhole limpet CC enacted with glutathione to produce a mercuric ion coordinate CC covalent compound which was covalently bound to keyhole limpet CC enacted with glutathione to produce a mercuric ion coordinate CC covalent compound which was covalently bound to keyhole limpet CC enacted with glutathione was covalently bound to keyhole limpet CC enacted with glutathione was solated from hybridoma cells with CC glundine isothiocyanate. First strand cDNA synthesis was cattalysed CC were complementary to the 5' end of the CHI domain of the heavy CC the C kappa domain. Some of the primers used for cDNA synthesis are CC chain expressed by the hybridoma of interest, or to the 5' and of CC the C kappa domain. Some of the primer used for cDNA synthesis are CC crafable region of a particular antibody polypeptide was also used CC an appropriate V-region primer. In addition, the VH primer Q97518 CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences CC in Q97488-Q97510 and the deduced AA sequences in R7921-R79250 & CC R78970-R78971. The descriptions of the SEO ID nos given on pp 44-45 cc used here.

CC used here.
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Best Local :
                                                                                                    R79247;
21-DEC-1995 (first entry)
Light chain variable region for monoclonal antibody 1F10.
Monoclonal antibody; heavy metal; mercury; variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide(s) which bind heavy metals, esp. mercury - derived monoclonal antibodies, used for detecting, removing, adding or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Light chain variable region for monoclonal antibody 5B6 Monoclonal antibody; heavy metal; mercury; variable reg
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21-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or formation of a specific Sequence 90 AA;
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                                                                                                                                                                                                                                                                                                                                                                                 Local
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mes 8; Conse
                                                                                                                                                                                                                                                                                        esedfvdyy
                                                                                                                                                                                                                                          ESEDFVAYY
                                                                                                                        standard; Protein; 107
                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
                                                                                                                                                                                                                                                                                                                                              94.18;
larity 88.98;
Conservative
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US-187407
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                                                                                                                                                                                                                                                                                                                                        Score 64; DB 14;
Pred. No. 2.34e+01;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bond within a mol.
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Pred.
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2.34e+01;
                                                                                                                                                                                                                                                                                                                                                                                               Length 107
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CC laim 23; Page 62; 105pp; English.

CC Hybridoma antibodies have been produced with the spleen cells of CC Hybridoma shibodies have been produced a mercuric ions of mercuric ions of reacted with glutathione to produce a mercuric ion coordinate CC covalent compound which was covalently bound to keyhole limpet the heavy straint glutathione to produce a mercuric ion coordinate CC themocyanin (KLH). Eight hybridomas (IFIO, 4AIO, ICLI, 564, 23F8, 2D5, 586 and 3E8) were producing MAbs that were strongly positive against glutathione expressed by the producing MAbs that were strongly positive against glutathione at the complementary to the 5° and of the CH domain of the carlysed CC were complementary to the 5° and of the CH domain of the heavy CC chain expressed by the hybridoma of interest, or to the 5° and of CC the C kappa domain. Some of the primer used for cDNA synthesis are CC variable region of a particular antibody polypeptide was also used CC variable region of a particular antibody polypeptide was also used CC and appropriate V-region primer. In addition, the VH primer Q97518 CC was used to amplify the mab 2D5 and 586 heavy chains. The sequences CC in G97498-Q97510 and the deduced AA sequences in R79241-R79250 & CC and in the claims are different from the descriptions in the sequence listings. The descriptions of the SEQ ID nos given on pp 44-45 cused here.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches
                                                                                                                                               03-AUG-1995.
27-JAN-1995; U01199.
27-JAN-1994; US-187407.
(BION-) BIONEBRASKA INC.
Lopez O, Wagner FW, Wylie DI
WPT: 95-275415/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-1995.
27-JAN-1995, U01199.
27-JAN-1994; US-187407.
(BION-) BIONEBRASKA INC.
Lopez O, Wagner FW, Wy:
WPI: 95-275415/36.
 Hybridoma antibodies have been produced with the spleen cells c BALB/C mouse that had received multiple injections of mercuric reacted with glutathione to produce a mercuric ion coordinate covalent compound which was covalently bound to keyhole limpet
                                                                  New polypeptide(s) which bin monoclonal antibodies, used neutralising heavy metals Claim 23; Page 66; 106pp; En
                                                                                                                                    WPI; 95-275415
N-PSDB; Q97507
                                                                                                                                                                                                                                                    Synthetic.
WO9520607-A.
                                                                                                                                                                                                                                                                                                     21-DEC-1995 (first entry)
Light chain variable region for monoclonal antibody 5G4
Monoclonal antibody; heavy metal; mercury; variable reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
W09520607-A.
                                                                                                                                                                                                                                                                                       light chain.
                                                                                                                                                                                                                                                                                                                                                          R79250;
                                                                                                                                                                                                                                                                                                                                                                        R79250 standard; Protein; 107
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Similarity 88.9%;
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
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                                                                                                                     bind
                                                                    English
                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 64; DB 14; Le
Pred. No. 2.34e+01;
0; Mismatches 1;
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                                                                                                 heavy metals,
or detecting, ı
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                                                                                                   adding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches
                                                                                                                                                                                                                (CAMB-) CAMBRIDGE ANTIBODY.
(MEDI-) MED RES COUNCIL.
MCCAfferty J, Pope AR, Johnson K
Jackson RH, Holliger KP, Marks J
Winter GP, Bonnert TP;
WPI; 92-056862/07.
                                                                                                                                                                                                                                                                                                                       WO9201047-A.
23-JAN-1992
10-JUL-1991; G01134.
10-JUL-1990; GB-011198.
19-OCT 1990; GB-022845.
12-NOV-1990; GB-024845.
06-MAR-1991; GB-004744.
15-MAY-1991; GB-010549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 564, 2378, 2D; 5B6 and 3E8) were producing Mabs that were strongly positive against glutatione-mercuric ions but negative against glutathione without mercuric ions. RNA was isolated from hybridoma cells with guanidine isothiocyanate. First strand cDNA synthesis was catalysed
display package.

Example 46; Fig 52; 109pp; English.

The sequence is the light chain of clone MIF encoding an scFv fragment specific for both hen and turkey egg lysozyme (HEL and TEL).

The DNA encoding the chain was amplified from a cDNA library prepd. from the spleen of an unimmunised mouse. The corresponding heavy chain was also amplified from an existing construct, pSWI-VHD1.3 (Ward et al. 1989). The two fragments were assembled via a linker to prepare an scFv construct which was ligated into the fdCAT2 vector for expression on the surface of fd bacteriophage. In this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pilus; g3p; bindi
specific binding
                                                                                                                                                                             Producing members of specific recombinant host cells with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-MAY-1992 (first entry) ight chain of Mlf clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacteriophage; gene III; filamentous; phagemid; capsid; coat;
us; g3p; binding; adsorption; gene VIII; diverse repertoire;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             esedfvdyy 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein; 108 AA
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larity 88.98;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR2
89..96
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
25..34
/label- CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ing; adsorption; gene VIII; diverse pairs; replicable genetic display
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
0; M
                                                                                                                                                                             binding pairs - by expression secreting replicable genetic
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. No. 2.34e+01;
Mismatches 1;
                                                                                                                                                                                                                                                    Hoogenboom HRJ, Griffi
Clackson TP, Chiswell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 107;
                                                                                                                                                                                                                                                      Griffiths iswell DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             package
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Best Loc
Matches
W02280; standard; Protein; 243 AA.
W02280;
29-OCT-1996 (first entry)
520C9 anti-c-erbB-2 two single chain Fv construct.
520C9; anti-c-erbB-2 monoclonal antibody; single chain construct; polypeptide linker; C-terminal amino acid sein vivo imaging; drug targetting experiment; homodimer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 40-41; 68pp; English.

The pref. vector or plasmid of the invention has a double-stranded DNA seq. coding for a variable region of a light or heavy chain of IGG, or for a variable region of a light or heavy chain of a immunoglobulin specific for an enzyme or surface protein. The sequence esp. codes for a variable region of a light chain having in the protein of a variable region of a light chain having sep. including the D region of the heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moore KW, Zaffaroni A;
WPI; 83-772290/39.
N-PSDB; N30165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SCHE )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-1992 (first entry)
Sequence of the leader, variable region and first 16 AAs of
the constant region of the Kappa-chain (light chain) of MOPC41.
Diagnosis; therapy; immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-1982;
05-DEC-1983;
                                                                                                                                                                                                                                                                                                                                                   101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P30251 standard; peptide; 146 P30251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LO-MAR-1983;
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                                                                                                                                                                                                                                                                                                                                                                                                  h 94.1%;
Similarity 88.9%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHERING CORP.
DNAX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                med expression vectors or plasmid(s) - with double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; US-358414.
; US-558551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= v
131..146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leader
                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 4;
Pred. No. 2.34e+01
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 64;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; L
2.34e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>;</u>
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                              sequence;
                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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antigen for imaging or treating breast or ovarian cancer etc. Sclaim 4; pages 60-61; 87pp; English.

C c-erbB-2 refers to a protein antigen expressed on the surface of tumour cells. such as breast and ovarian tumour cells, which is an 2C approx. 200,000 mol. wt. acidic glycoprotein having an isolelectric pt. of about 5.3 (see Q46083, R39568). A single chain Fv (sFv) class a covalently linked VH-VL heterodimer which is expressed from a gene fusion including VH- and VL- encoding genes connected by ca peptide-encoding linker. Such linker sequences are set forth in 2C a peptide-encoding linker. Such linker sequences are set forth 1 claim for the 16 AA collinker sequences in R39572. Using Q46084 for the 520C9 monoclonal claim for the 16 AA collinker sequences in R39572. Using Q46084 for the 520C9 monoclonal claim for the 520C9 monoclonal collinker sequences are set forth in 2C antibody, a single chain polypeptide can be produced having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
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Example 1; Columns: 33-36; 30pp; English.

CC Variable heavy (VH) and variable light (VL) genes were cloned from cc antibody constant and joining regions. A two single chain Fv (sFv) columns was constructed by connecting the VH and VL genes with a cc gene was constructed by connecting the VH and VL genes with a cc which encodes the present sequence, was inserted into an expression cc westor, transformed into E. coll, and protein expression induced by compsn. compsising a carrier and the 2 sFv protein prod. Is a homodiner, in which both fragments target the same antigen, therefore giving greater binding avidity and cc longer tissue retention times, compared to individual sFv protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
Matches
                                                                                                                                                                                         New single chain Fv polypeptide binding tantiqen - for imaging or treating breast
                                                                                                                                                                                                                                            (CETU ) CETUS ONCOLOGY CORP.
(CREA-) CREATIVE BIOMOLECULES INC.
HOUSTON LI. HUSTON JS, Oppermann H,
WPI: 93-272889/34.
                                                                                                                                                                                                                                                                                                           19-AUG-1993.
05-FEB-1993; U01055.
06-FEB-1992; US-831967
                                                                                                                                                                                                                                                                                                                                                                                        Sequence of 520C9 sFv protein.
Single chain Fv polypeptide; VH-VL
biosynthetic single polypeptide cha
                                                                                                                                                                                                                                                                                                                                                                                                                                               R39569 standard; Protein;
R39569;
07-FEB-1994 (first entry)
                                                                                                                                                                                                                                N-PSDB; Q46084
                                                                                                                                                                                                                                                                                                                                                             WÓ9316185-A.
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR) CHIRON CORP.
(CREA-) CREATIVE BIOMOLECULES INC.
HOUSTON LL, HUSTON JS, Oppermann
WPI; 96-333194/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-1996.
06-FEB-1992; 831967.
06-FEB-1992; US-831967.
07-OCT-1993; US-133804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 esedfvvyy 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-PSDB; T36880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     increased; binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESEDFVAYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.1%;
larity 88.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
118..133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   avidity; tissue retention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
0; M
                                                                                                                                                                                                                                                                                                                                                                                      -VL heterodimer; immunoglobulin;
chain binding site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64; DB 18;
No. 2.34e+01;
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                                                                                                                                                                                                                                                          Ring
                                                                                                                                                                                      or or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ring
                                                                                                                                                                                                         C-erbB-2
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                                                                                                                                                                                                          tumour
                                                                                                                     isolelectric
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  ဥ္ပင္သ
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches
                             JO-MAR-1994; JP-082693.

(TAKI ) TAKARA SHUZO CO L

Atsushi O, Hirofumi Y,

WPI; 95-338286/44.

N-PSDB; T04179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.

W0931618-A.

19-AUG-1993.

05-FEB-1993; U01055.

06-FEB-1992; US-831967.
                                                                                                                                                                                                                                                                                                                                                                                   antigen for imaging or treating breast or ovarian camerater.

Example, pages 65-68; 87pp; English.

C-erbB-2 refers to a protein antigen expressed on the surface of tumour cells. such as breast and ovarian tumour cells, which is an approx. 200,000 mol. wt. acidic glycoprotein having an isolelectric pt. of about 5.3 (see Q48083, R39568).
Gene encoding variable region of anti-human influenza antibody - useful for prodn. of artificial antibodies Example 4; Page 33-35; 42pp; English.
                                                                                                                                                                                                      C179Fv-PP variable light chain sequence. Antibody; human; influenza type A virus; H1N1; haemagglutinin; variable light chain; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New single chain Fv polypeptide binding tantigen - for imaging or treating breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; Q46086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CETU ) CETUS ONCOLOGY CORP.
(CREA-) CREATIVE BIOMOLECULES INC.
HOUSTON LL, HUSTON JS, Oppermann
WPI: 93-272889/34.
                                                                                                                                domain
                                                                                                                                                     domain
                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                              R92829 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 10
R39571 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             refers to the location
                                                                                       14-MAR-1995;
                                                                                                            EP-675199-A2.
                                                                                                                                                                          protein
                                                                                                                                                                                                                                         09-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-1994 (first
                                                                                                                                                                                                                                                                                                                             503 esedfvvyy 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 esedfvvyy 220
                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                         ESEDFVAYY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESEDFVAYY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of G-FIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 AA;
                                                                                                                                                                                                                                                                                                                                                   94.1%;
larity 88.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.18;
larity 88.98;
Conservative
                                                                                     301664
                                                                                                 /note= "FC Dinum;
194..251
/note= "Fc binding domain-like structure"
                                                                                                                                                    /note= "\
136..193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c-erbB-2; G-FIT
                                                                                                                                                                        26..126
                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             t c-erbB-2 r
                                                                                                                                                              "variable light chain"
                                                    IKunoshin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    534 AA
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                                                                                                                                                                                                                                                                                                                                                 Score 64;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
0; M
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p codon in Q46084
                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ή
                                                                                                                                                                                                                                                                                                                                                             DB 8; Lt 2.34e+01;
                                                       Takashi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8;
2.34e+01
                                                                                                                                                                                                                                                                                                                                                                                                                                                           to C-erbB-2
; or ovarian
                                                                                                                                                                                                                                                                                                                                                                      Length 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                   H2N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour
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                                                                                                                                                                                                                   H3N2;
                      type virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R39569
                                                                                                                                                                                                                                                                                                                                                   0
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                                                       0
                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                   diagnosis;
                                                                                                                                                                                                                                                                                                                                                   0
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Š 밁

99

ESEDFVAYY

107

238 qaedfvsyy 246

Mismatches

0;

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         문
                                                                                  Fig. Gene encoding variable region of anti-human influenza A type virus produced for file sequence represents the scFv-PP fusion polypeptide. This sequence files and files for produced for files for produced for files for produced for files for files for produced for files files for files for files for files for files for files files for files files for files for files for files for files for files files for files files files files for files files files files for files fi
Query Match
Best Local S
Matches
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Atsushi O, Hiro
WPI; 95-338286/
N-PSDB; T04180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-1995.
14-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCFV-PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R82835 standard;
R82835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haemagglutinin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TAKI ) TAKARA SHUZO CO
Atsushi O, Hirofumi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-1995; 301664.
30-MAR-1994; JP-082693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 qaedfvsyy 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 89.7%;
Similarity 66.7%;
6; Conservative
h 89.7%;
Similarity 66.7%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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331..388
/note= "I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "1
273..330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164..263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  influenza type A virus; H1N1; rariable heavy chain; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "variable heavy chain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Fc binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "variable light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITD.
Ikunoshin
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Score
Pred.
3; M
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Pred.
3; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                       61; DB 16;
No. 4.22e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61; DB 16;
No. 4.22e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain-like structure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ŧ,
                                               Length 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H2N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   influenza A type virus antibody. The antibody recognises the stem region of the haemagylutinin (HA) molecule of the HIN1 and HAN2 subtypes of human influenza A type virus, and shows neutralisation activity against these two subtypes. The antibody shows no recognition of the HIN2 subtype. The DNA encoding this sequence and the variable hevay chain coding sequence (see T04159) are useful in the production of artificial antibodies and antigen-binding polypeptides. These artificial antibodies and encigen-binding polypeptides. These artificial antibodies influenza. As the antibodies recognise the stem region of the HA molecule, the influenza virus will be recognised even if the HA molecule changes. This provides an advantage over current vaccines, as the virus sequence of the hamperiodically alters it's HA molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                           LT 14
R80079 standard; Protein; 90 AA.
R80079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           periodically area
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene encoding variable region of anti-human influenza A type antibody - useful for prodn of artificial antibodies Claim 2: Page 20; 42pp; English.
This sequence represents the variable heavy chain region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region
                             region
                                                                         region
                                                                                                                    region
                                                                                                                                                                   region
                                                                                                                                                                                                                                                                                                                                 pattern
                                                                                                                                                                                                                                                                                                                                                     Mouse derived light chain; RT3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-1994; JP-082693.
(TAKI ) TAKARA SHUZO CO
Atsushi O, Hirofumi Y,
WPI; 95-338286/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-1996 (first entry)
Variable light region of the anti-human influenza A type virus antibody.
Antibody: human; influenza type A virus; H1N1; H2N2; H3N2; H3, diagnosis;
                                                                                                                                                                                                                 region
                                                                                                                                                                                                                                                             region
                                                                                                                                                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 95-338286/44.
N-PSDB; T04160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haemagglutinin; variable heavy chain; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESEDFVAYY 107
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                       light chain
RT3; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
                                                                                                             /note=
27..40
/note=
41..47
                                                                         /note-
48..78
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50..55
/label= CDR2
                          /note=
79..88
                                                                                                                                                                                                               /note=
16..26
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                                                                                                                                                                                                                                                                                Location/Qualifiers
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55.68;
                                              "framework region
                                                                                                                                                                                                                                *framework region
  "complementarity
                                                                                     "complementarity determining
                                                                                                                                      "framework region 2"
                                                                                                                                                                                    "complementarity determining
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                                                                                                                                                                                                                                                                                                                                                  RT3 phage catalytic
                                                                                                                                                                                                                                                                                                                                                                                RT3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58; D. Pred. No. 7. 4; Mismatcl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                  antibody pattern C.
antibody; bacteriophage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; 17.56e+01; 0;
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determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Best Local Similarity
Matches 7; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09527045-A1.
12-OCT-1995.
30-MAR-1994; U03420.
30-MAR-1994; WO-U03420.
(IGEN-) IGEN INC.
New human monoclonal antibodies to hepatitis C virus E2 antigen obtained using a combinatorial antibody library prepared using RNA from a HCV infected subject, useful for vaccine preparation claim 5; Fig 2E; 103pp; English.

The present sequence represents the alpha light chain peptide sequence of the Fab molecule, clone L1. This immunoglobulin molecule is capable of specifically binding with the hepatitis C virus (HCV) E2 antigen. The present sequence was obtained from a combinatorial antibody library. The alpha light chain peptide can be used to construct a recombinant human monoclonal antibody (MAb). The monoclonal antibodies exhibit immunological binding affinity for HCV E2 antigen and are cross-reactive with different HCV strains. They can be used to produce vaccine compositions which can be used to provide antibodies to HCV in a subject or to provide passive immunity or to treat HCV infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-APR-1998 (first entry)
Alpha light chain amino acid sequence of the Fab molecule clone Alpha light chain; Fab molecule; binding; hepatitis C virus; HCV E2 antigen; combinatorial antibody library; vaccine; antibody; recombinant human monoclonal antibody; immunological binding aff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacteriophage. The CAS can be well be enhancing the rate biological function in an animal by enhancing the rate or formation of a specific bond within a mol. in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T04626 encodes R80079 mouse derived in the preph. of catalytic antibody (CA) The DNA was used in the preph. of catalytic antibody the bacteriophage. The CAs can be used to activate/deactivate bacteriophage. The case of the catalytic antibody (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Production of catalytic antibodies displayed on phage - by generating a gene library of antibody-derived domains and it in phage vectors
Disclosure; Fig 9; 133pp; English.
T04626 encodes 80079 mouse derived light chain RT3 phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-1997; E01977.
17-APR-1997; US-844215.
19-APR-1996; US-635109.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Allander TE, Persson MA; WPI; 97-535857/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PERS/) PERSSON M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9740176-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-1997;
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50..56
/note=
89..97
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Pred. No. 9.17e+01;
0; Mismatches 2
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f cleavage,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HCV;
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CC subjects. They can also be used to detect HCV and to monitor anti-HCV CC therapeutic treatment.

CC note: this sequence is allegedly encoded by T88837; however, the cc peptide encoded by that nucleotide sequence differs considerably to the CC present peptide.

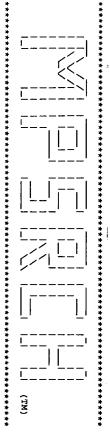
SQ Sequence 107 AA;

Ouery Match 83.8%; Score 57; DB 28; Length 107; Best Local Similarity 77.8%; Pred. No. 9.17e+01; Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0; DB 79 esedfavyy 87 99 ESEDFVAYY 107

Search completed: Tue Apr 20 14:01:59 1999

Search completed: Tue Apr 20 14:01:59 1999
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

abular output not generated. n on: Tue Apr 20 14::01:07 1999; MasPar time 3.31 Seconds $$^{\rm h}$$ ----101.886 Million cell updates/sec

Description: Perfect Score: Title: >US-08-836-455-2 (99-107) from US08836455.pep (3 of 3)

1 ESEDFVAYY 9

PAM 150 Gap 11

Scoring table:

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir58 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 25.001; Variance 40.079; scale 0.624

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	s	4	ω	2	ם	sult No.
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RESULT 2 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors	Query Match Best Local Simila Best Local Simila Watches 8; C Matches 1 1 1 1 1 Oy 99 ESEDFVAYY	17-50 1-50 6-16 17-31 32-38 39-70 71-79 80-88 SUMMARY	#accession Pt0261 ##molecule_type mRNA ##molecule_type mRNA ##residues 1-88 CLASSIFICATION #superfam KEYWORDS heterotet	#journal #title #cross-referen	TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors
PLO260 #type fragment Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment) #formal_name Mus musculus #common_name house mouse 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996 PLO260 PLO231 Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,	Similarity 88.9%; Score 64; DB 2; Length 88; Similarity 88.9%; Pred. No. 4.48e-01; 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0; EDFVDYY 69	<pre>#region framework 1\ #region complementarity-determining 1\ #region framework 2\ #region complementarity-determining 2\ #region framework 3\ #region framework 3\ #region complementarity-determining 3\ #region framework 4 #region framework 4</pre>	PLO261 type mRNA 1-88 ##label SHL superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin	Marshak-Rothstein, A.; Welgert, M. Med. (1990) 171:265-297 NA antibodies from autoimmune mice arise by clubion and somatic mutation. ID:90111618	PLO261 #type fragment. Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment) If kappa chain V region (anti-DNA, DP15VK) - mouse (fragment) If chair ends was musculus #common_name house mouse 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997 PLO261 PLO261 PLO231 Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,

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D.; Marshak-Rothstein, A.; Weigert, M.
#journal J. Exp. Med. (1990) 171:265-297
#title Anti-DNA antibodies from autoimmune mice arise expansion and somatic mutation.
#cross-references MUID:90111618
#accession PL0259
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#title Anti-DNA antibodies from autoimmune mice arise
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RDS heterotetramer; immunoglobulin
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 KVMSM4 *type complete
If kappa chain precursor V region (MOPC 41) - mouse
If kappa chain precursor V region VK41
kappa chain precursor V region VK41
*formal_name Mus musculus *common_name house mouse
24-Apr-1984 *sequence_revision 24-Apr-1984 *text_c)
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#formal_name Mus musculus #common_name house mouse
16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
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##molecule_type protein

##residues 23-49,'B',51-53,'LSB',57-58,'ZZ',61-62,'BZ',65-76,'B',

##residues 78-108,110-130 ##label GRA
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#journal Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720
#title Amino acid sequence of the NH-2-terminal extra piece segments
of the precursors of mouse immunoglobulin lambda-1-type and
#cross-references MUID:77148916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors Seidman, J.G.; Max, E.E.; Leder, P.
#journal Nature (1979) 280:370-375
#title A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.
#cross-references MUID:79221900
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H30502 #type complete
If kappa chain V region (D42) -
#formal_name Mus musculus #commo
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A93211
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                                                                                                                                                                                                                                             experimental #label M41\
#domain immunoglobulin homology #label IMM\
#disulfide_bonds #status predicted
#th 130 #molecular-weight 14311 #checksum
                                                                                                                                                                                                                                                                                                                *product Ig kappa chain V region (MOPC 41) *status
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from NZB/NZW F-1 mice.
#cross-references_MUID:88315787
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##cross-references GB:M21912; NID:g197077; PID:g197078
##cross-references GB:M21912; NID:g197077; PID:g197078
##cross-references GB:M21912; NID:g197077; PID:g197078
#superfemily immunoglobulin
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heterotetramer; immunoglobulin
#idength 103 #molecular-weight 11280 #checksum
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Similarity 77.8%;
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Ig kappa chain V region (V-kappa 3) - human (fragment)
#formal_name Homo sapiens #common_name man
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
08-Sep-1997
S37510
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           Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
Human IgM(+)IgD(+) cells, the major B cell subset i
peripheral blood, expresses V(kappa) genes with I
little somatic mutation throughout life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Immunol. (1989) 142:3158-3163
Structural and idiotypic characterization of the L chains
human IgM autoantibodies with different specificities.
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Ig kappa chain V-III region (Bor) - human (
#formal_name Homo sapiens #common_name man
29-Jun-1989 #sequence_revision 29-Jun-1989
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1; M
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Pred. No. 1.48e+00;
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141:1745-1753
of anti-DNA and a
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No. 1.48e+00;
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A.; Mendez, E.;
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                                                                         ##experimental_source B cell, strain [NZB x NZW]F1
CLASSIFICATION #superfamily immunoglobulin V region; i
KEYWORDS immunoglobulin
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#journal
#title
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#FICATION #superfamily immunoglobulin V region; immunoglob

BOS heterotetramer; immunoglobulin

#Iength 92 #checksum 6347
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##molecule_type mRNA
##residues 1-92 ##label KLE
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##molecule_type nucleic acid
##residues
1-91 ##label CLA
IFICATION #superfamily immunoglobulin V region; immunoglobulin homology
RDS heterotetramer; immunoglobulin
RDS heterotetramer; immunoglobulin
RY #length 91 #molecular-weight 9895 #checksum 3446
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                                                                                                                       ##residues
                                                                                                                                   ##molecule_type mRNA
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              33.8%;
Similarity 77.8%;
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S17230
Clackson,
                                                                                                                                                                                Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N. J. Exp. Med. (1992) 176:761-779
Both IgM and IgG anti-DNA antibodies are the produclonally selective B cell stimulation in (NZB x mice.
                                                                                                                                                                                                                                                                                       PH1062 #type fragment
Ig 11ght chain V region (clone 202.105) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
15-Jun-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IS17622 #type complete
IG Kappa chain V region - mouse
#formal_name Mus musculus #common_name house mouse
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
                                                          immunoglobulin
#length 98 #cl
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77.8%;
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Pred. No. 4.74e+00;
2; Mismatches 1
Score 57; DB 2; Lo.
Pred. No. 6.94e+00;
Wismatches 2;
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Pred. No. 6.94e+00;
0; Mismatches 2
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57-88
89-97
98-106
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Best Local Similarity
Matches 7; Conser
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                                                                                                                                                                                                                                                                                         #authors Shlomchik, M.; Mascelli, M.; Shan, H.; Ra
D.; Marshak Rothstein, A.; Weigert, M.
#journal J. Exp. Med. (1990) 171:265-297
#title Anti-DNA antibodies from autoimmune mice
expansion and somatic mutation.
#cross-references MUID:90111618
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ESEDFVAYY 107
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|ESEDFVAYY
                                               h 83.8%;
Similarity 77.8%;
7; Conservative
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#superfamily immunoglobulin V region; immunoglobulin homology
                                                                                                    #length
                                                                                                                                                                                                                      heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                  PL026:
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1g kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
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larity 77.8%;
Conservative
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Ig kappa chain V region (HP27) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change
16-Aug-1996.
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framework 2\
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                                              Score 57; DB 2; I
Pred. No. 6.94e+00;
0; Mismatches 2
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Best Local Similarity 77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            #title Variation in the crossover point of kappa immunoglobulin gene V-J recombination: evidence from a cryptic gene. #cross-references MJD:81064681 #accession A01924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Lesley, S.A.; Patten, P.A.; Schultz, P.G.
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1160-1165
#title A genetic approach to the generation of antibodies with
enhanced catalytic activities.
#cross-references MUID:93165660
#accession B47271
                                                                                                                                                                                                                                                                                                                                   *#molecule_type DNA

##residues
1-117 ##label MAX

##cross-references GB:K00880; NID:g197443; PID:g197444

##note
the sequence was determined from the germline gene
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                                                           #length
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                                                                                                                                                                                heterotetramer
                                                                                                                                                                                        oligomers.
#superfamily immunoglobulin V region;
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Cell (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain precursor V region (VKM173B) - mouse #formal_name Mus musculus #common_name house mouse 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B4727
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                                                                                                                                                                                                                           immunoglobulin heterotetramer subunit consists of two identical light (Kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nitrophenyl phosphonate-specific antibody 48G7 light chain vJ
- synthetic (fragment)
#formal_name synthetic
Mus musculus (house mouse) gene engineered and expressed in
Escherichia coli
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                                             #domain signal sequence #status predicted #label SIG\
#product Ig kappa chain V region (VKM173B) #status
predicted #label MATV.
#disulfide_bonds #status predicted
#th 117 #molecular-weight 12954 #checksum 3822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-Aug-1995
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parts of this sequence were determined
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    83.8%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #type complete
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Pred. No. 6.94e+00;
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Pred. No. 6.94e+00;
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CLASSIFICATION
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Best Local :
                                                                         Query Match 82.4%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                         #authors #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #journal J. Clin. Invest. (1988) 82:852-860
Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice.
#cross-references_MUID:88331394
                                                                                                                                                                                                                                                                                   #accession
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                                                                                                                                         ##residues 1-82 ##label WAG
##cross references EMBL:X67174
##cross references immunoglobulin V region; immunoglobulin homology
IFICATION #superfamily immunoglobulin
ADS heterotetramer; immunoglobulin
ADS heterotetramer; immunoglobulin
ADS #length 82 #molecular-weight 8891 #checksum 4385
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Local Similarity 77.8%;
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ESEDFVAYY 107
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                                                                                                                                                                                                                                                                           Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. (1993) 23:391-397
V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V-kappa locus and do not show somatic mutation.
S34090
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S34076
                                                                                                                                                                                                                                                                                                                                                                                                                                                  334090 #type complete
Ig kappa anhain V region - human
#formal_name Homo sapiens #common_name man
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain precursor v region (BXW16) - mouse fformal_name Mus musculus fcommon_name house mouse 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.;
Noonan, D.J.; Duchosal, M.A.; Dixon, F.J.; Theofilopoulos,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A94689
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                                                                       Score 56; DB 2; I
Pred. No: 1.01e+01;
2; Mismatches 1
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Search completed: Tue Apr 20 14:01:25 1999 Job time : 18 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm on:

Tue Apr 20 13:59:47 1999; MasPar time 2.35 Seconds 102.676 Million cell updates/sec

Tabular output not generated.

Title: >US-08-836-455-2
Description: (99-107) from US08836455.pep (3 of 3)
Perfect Score: 68

Sequence: 1 ESEDFVAYY 9

Scoring table: PAM 150 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swissprot

Statistics: Mean 25.463; Variance 33.115; scale 0.769

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222118 232118 232118	sult No.
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94.1 82.4 82.4 82.4 79.4 79.4 79.4 77.9 77.9 77.9 77.9	Query Match
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Query Match Best Local Similarity

94.1%; 88.9%;

Score 64; DB 1; Length 130; Pred. No. 3.87e-02;

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53 53 55 55 55 55 55 55 55 55 55 55 55 5	5 5 3
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PO1603;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN V-I REGION (KA)
HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                 PIR; A01869; K1HUKA. HSSP; P01607; 1IGM.
                                                                                                                                                          MEDLINE: 76189985.

SHINODA T.:

J. BIOCHEM. 77:1277-1296(1975).

-!- THE C REGION OF THIS CHAIN HAS
-!- THIS IS A BENCE-JONES PROTEIN.

DID. A01860. FILL
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MAX E.E., SEIDMAN J.G., MI

CELL 21:793-799(1980).

EMBL; K00880; G197444; -...
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HSSP; P01607; 1FGV.
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MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -UUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
-OCT-1996 (REL. 34, LAST ANNOTATION UPDAT
KAPPA CHAIN PRECURSOR V-V REGION (MOPC 1
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77.8%;
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Pred.
0; M
                                 FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 3.
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              COMPLEMENTARITY-DETERMINING
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FRAMEWORK 1.
COMPLEMENTÄRITY-DETERMINING 1.
FRAMEWORK 2.
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1. No. 1.05e+00;
1-+-hes 2;
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(MOPC 173B).
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Best Local s
Matches
SEQUENCE FROM N.A.

MEDLINE: 84270667.

BAER R., BANKIER A.T., BIGGIN M.D.

GIBSON T.J., HATFULL G., HUDSON G.

TUFFNELL P.S., BARRELL B.G.;

NATURE 310:207-211(1984).

-i- FUNCTION: PRESUMED VIRION PROJ

PACKAGING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (REL. 01,
21-JUL-1986 (REL. 01,
01-DEC-1992 (REL. 24,
VIRION PROTEIN BBRF1.
                                                                                                                                                                                                                                                               UL06_EB
P03213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
NON_TER
SEQUENCE
                                                                                                                                              EPSTEIN-BARR VIRUS (STRAIN
VIRIDAE; DS-DNA ENVELOPED V
                                                                                                                                                                                    BBRF
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DISULFID
NON_TER
SEQUENCE
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21-JUL-1986 (REL. 01, LAST SEQUENCE UI
01-JAN-1988 (REL. 06, LAST ANNOTATION
IG KAPPA CHAIN V-I REGION (OU).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 70201507
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                                                                                                                                                                                                                                                                                 EBV
                                                                                                                                                                                                                                                                                                                                           ESEDFVAYY 107
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                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                               CREATED)
                                                                                                                                                                                                          LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                              N B95-8) (
VIRUSES;
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Pred. No.
5; Misma
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Pred. No. 1.65e+00
5; Mismatches
                  PROTEIN;
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERTEBRATA; TETRAPODA; MAMMALIA;
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BY SIMILARITY
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                                                                G.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4B089785 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                           (HUMAN HERPESVIRUS
HERPESVIRIDAE; GA)
                                                             DEININGER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE INV (3) MARKER.
WALDENSTROM'S MACROGLOBULIN.
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                  ROLE
                                                                                                                                           GAMMAHERPESVIRINAE
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                                                             FARRELL P.J., ., SEGUIN C.,
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KV1K_HUMAN

Matches Query Match Best Local

Local Similarity

101

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21-JUL-1986 (REL. 21-JUL-1986 (REL. 01-OCT-1996 (REL.

SEQUENCE FROM N.A.

KV5H_MOUSE P01641;

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ESEDFVAYY 107 ESEDEVDYY Matches

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TRESULT AND THE SOLUTION OF TH
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Best Local s
Matches
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Best Local
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MILSTEIN C.P., DEVERSON E.V.;
EUR. J. BIOCHEM. 49:377-391(1974).
-!- THE C REGION OF THIS CHAIN HAS THE INV (1
-!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PR PIR; A01864; KIHUAR.
HSSP; P01607; 1DFB.
IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: BELONGS TO EHV-1 56, EBV BBRF1, H EMBL; V01555; G59125; -. PIR; A03775; QQBE33. PIR; S33025; S33025. LATE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KV1D_HUMAN
P01596;
                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                             KV3C_HUMAN
P01621;
                                                                                 NATURE 307:77-80(1984).
-:- THIS GENE WAS ISOLATED PIR; A01894; K3HUMC.
HSSP; P01607; LAAG.
HSSP; P01607; LAAG.
                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 84093600. BENTLEY D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UF
21-JUL-1986 (REL. 01, LAST ANNOTATION
IG KAPPA CHAIN V-I REGION (CAR).
      DISULFIL
                          CHAIN
                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SKOUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST SKOUENCE UPDATE)
1G KAPPA CHAIN PRECURSOR V-III REGION (NG9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 SDEYVAYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 SEDFVAYY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 ZPBBFATYY 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESEDFVAYY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 33.3%, 3; Conservative
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Similarity 62.5%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
107
107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                613 AA;
      27 5 A 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
    100
93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11703 MW;
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                                                                                   SIGNAL;
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                                                                                                                                                   FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55;
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Pred.
3; M
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KAPPA CHAIN V-III REGION (NG9).
SIMILARITY.
                                                                                                                                                   THE NG9/9.1
                                                                                   HYBRIDOMA
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                                                                                                                                                                                                                                                                                                                                         UPDATE)
(NG9) (FRAGMENT).
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2.58e+00;
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PROTEIN.
                                                                                                                                                   HYBRIDOMA
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Best Local S
Matches
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Best Local
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PO1624;

21-JUL-1986 (REL. 01, CREATED)

21-JUL-1986 (REL. 01, LAST SEC

20-MAR-1987 (REL. 04, LAST AND

IG KAPPA CHAIN V-III REGION (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KV3A_HUMAN STAN
P01619;
21-JUL-1986 (REL. (
21-JUL-1986 (REL. (
20-MAR-1987 (REL. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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HSSP; P01607; 1DFB.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLAPPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLAPPER D.G., CAPRA J.D.;
ANN. INST. PASTEUR IMMUNOL.
-!- THIS CHAIN WAS ISOLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLAPPER D.G.,
ANN. INST. PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA; PRIMATES
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Local Similarity 66.7%;
99
                                                           80 QSEDFAVYY 88
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ESEDFVAYY 107
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109 AA;
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01, LAST SEQUENCE U
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10729 MW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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                                                                                                                       Score 54; DB 1; Lei
Pred. No. 4.01e+00;
1; Mismatches 2;
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Pred. No. 4.01e+00;
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FROM AN IGM WITH ANTI-GAMMA GLOBULIN
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MEDLINE; 72188439.

SUTER L., BARNIKOL H.U., WATANABE S., HILSCHMANN HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 353:189-208(1977).

--- THE C REGION OF THIS CHAIN HAS THE INV (3) M.

--- THIS IS A BENCE-JONES PROTEIN.

PIR; A01895; K3HUTI.

PIR; A01895; K3HUTI.

R HSSP; P01607; 21MM.

IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.

KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                          Query Match
Best Local
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Best Local S
Matches
       KV3G_HUMAN
P04206;
20-MAR-1987
20-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
SEQUENCE.
SEQUENCE.
SEQUENCE.

MEDLINE; 82046598.

ANDREWS D.W., CAPRA J.D.;
BIOCHEMISTRY 20:5816-5822(1981)....

BIOCHEMISTRY 20:5816-5822(1981)....
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P01623;
21-UUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN V-III REGION (WOL).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                            IMMUNOGLOBULIN V REGION.
DISULFID 23 89
NON_TER 109 109
SEQUENCE 109 AA; 1174
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P01622;
P01622;
21-UUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN V-III REGION (TI).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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                                                                                                                                                                                                    EPEDFAVYY
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                                                                                                                                                                                                                                                               Similarity 66.7% 6; Conservative
    (REL.
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109
109 AA;
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                                                                            STANDARD;
04, CREATED)
04, LAST SEQUENCE
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11746
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11788 MW;
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CHAIN HAS THE INV (3) MARKER.
                                                                                                                                                                                                                                                     Score 54; DB 1; Leg
Pred. No. 4.01e+00;
1; Mismatches 2;
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Pred. No. 4
1; Mismat
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UPDATE)
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Best Local
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Best Local S
Matches
                                                                                                            KV31_HUMAN STANDARD;
P04433;
13-AUG-1987 (REL. 05, CREA:
13-AUG-1987 (REL. 05, LAST:
01-NOV-1990 (REL. 16, LAST:
1G KAPPA CHAIN PRECURSOR V
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDA:
EUTHERIA; PRIMATES.
SEQUENCE FROM N.A. MEDLINE; 85087932. PECH M., ZACHAU H.
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. BICCHEM. 73:433-446(1973).
J. BICCHEM. 73:433-446(1973).
J. BICCHEM. 73:433-446(1973).
J. THE C REGION OF THIS CHAIN HAS THE INV (1974).
J. THIS IS A BENCE-JONES PROTEIN.
PIR, A01880, KIHUNY.
HSSP; P01607; IFVD.
IMMUNOCLOBULIN V REGION; BENCE-JONES PROTEIN IMMUNOCLOBULIN V REGION V REGIO
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SHINODA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JAN-1988 (REL. 06, LAST AUNOTATION UPDATE)
IG KAPPA CHALN V-I REGION (NI).
HUMO SAPIENS (HUMAN),
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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SEQUENCE
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETR
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|:||| ||
99 ESEDFVAYY 107
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MEDLINE; 86230578.
NEWKIRK M., CHEN P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 ZPZBFAVYY
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ISSP: P01607; 1DFB.
IMMUNOGLOBULIN V REGION.
23 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
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Local Similarity 33.3%;
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6; Conservative
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112 AA;
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109 1
109 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
                                                                                                                                                                        .. 05, CREATED)
L. 05, LAST SEQUENCE UPDATE)
L. 16, LAST ANNOTATION UPDATE
TOTOGOR V-III REGION (VG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112
.; 12246 MW;
                                                                                                                                    CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54; DB 1; I
Pred. No. 4.01e+00;
4; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D.A.,
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No. 4.01e+00;
                                                                                                                                                                                                                                                                                                                                             115
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                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                 TETRAPODA; MAMMALIA;
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Best Local (
                                              Query Match 79.4%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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DISULFID
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DOMAIN
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DOMAIN
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KY3K_HUMAN STANDARD; PRT; 128 AA.

P06311;

01-JAN-1988 (REL. 06, CREATED)

01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)

01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)

1G KAPPA CHAIN PRECURSOR V-III REGION (IARC/BL41).

HOMO SAPIENS (HUMAN).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEIC ACIDS RES. 12
EMBL; X01668; -; NOT
PIR; A01900; K3HUVG.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 86041852.
KLOBECK H.G., MEINDL A., COMBRIATO G.;
NUCLEIC ACIDS RES. 13:6499-6513(1985).
EMBL; 200021; G33179; -
EMBL; 200029; K3HU41.
PIR; A01899; K3HU41.
HSSP; P01607; 3HFM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                  MMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 79.4%;
Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 ESEDFVAYY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 EPEDFAVYY 107
  99 ESEDEVAYY 107
                        99 EPEDFAVYY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                 21
24
55
70
                                                                                                                                                                                                                                                  V REGION; SIGNAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12:9229-9236(1984)
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43
54
76
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117
128
108
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                                                                                                  14070 MW;
                                                                                                                      IG KAPPA CHAIN V-III REGION (IARC/BL41).
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.
JK1 SEGMENT.
BY SIMILARITY.
                                              Score 54; DB 1; Length 128; Pred. No. 4.01e+00; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54; DB 1; Length 115; Pred. No. 4.01e+00;

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY-DETERMINING 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG KAPPA CHAIN V-III REGION (VG).
                                                                                                  318E08AF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37E182FC CRC32;
                                                                                                                                                                                                                                                                                                              SOLOMON A., ZACHAU H.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                 0
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                                                 Gaps
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Search completed: Tue Apr 20 13:59:53 1999 Job time : 6 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Tue Apr 20 14:00:10 1999; MasPar time 4.37 Seconds 102.577 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-836-455-2 (99-107) from US08836455.pep (3 of 3) 68

ESEDFVAYY 9

Scoring table: PAM 150 Gap 11

Searched: 165420 segs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 24.693; Variance 34.950; scale 0.707

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19 20	17 18	16	15	14	13	12	11	10	9	œ	7	6	5	4	ω	2	<u> </u>	Result
53 3	5 5 5	53	53	53	53	53	54	54	54	54	54	54	54	54	56	56	56	Score
77.9 77.9	77.9		77.9	77.9		77.9	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	82.4	82.4	82.4	Query Match I
217	113 4	112 '	105 ′	94 ,	93 ,	81 1:	504	504 1:	504 4	251	115 4	114 /	113 4	108 4	772 11		236	Length DB
1 015358 5 Q27277	014540	1 099822	1 099514	1 016079	1 016078	L Q61588	5 Q27968	L Q60873	1 Q13217	3 042983	1 014537	1 014538	014539	1 099818	L Q62711	L Q63693	P95945	Ħ
40	J. U		_	_	~	~	~	~	_	_	-	~	_	~	•	_	٠.	i
															-	<u>.</u>		 #******* ********
IMMUNOGLOBULIN VARIABL Y-BOX BINDING PROTEIN	HRV FAB 027-VL (FRAGMEN HRV FAB N6-VL (FRAGMEN	I-HIV-1 GP12	z	RF-V KAPPA 1-RHEUMATOI	RF-V KAPPA 1-RHEUMATOI	G8(ANTI-MRBC HYBRIDOMA	PKR INHIBITOR P58.	PROTEIN KINASE, INTERF	PROTEIN KINASE INHIBIT	HYPOTHETICAL 28.9 KD P	HRV FAB N27-VL (FRAGME	: HRV FAB N28-VL (FRAGME	'! HRV FAB 026-VL (FRAGME	ANTI-SSDNA ANTIBODY LI	PHOSPHOLIPASE C DELTA-	PHODPHOLIPASE C DELTA4	ENDONUCLEASE III.	Description

45	44	43	42	41	40	39	38	37	36	ω S	34	ω ω	32	<u>3</u> 2	30	29	28	27	26	25	24	23	22	17
49	50	50	50	50	50	50	51	51	51	51	52	52	52	52	52	52	52	52	52	52	52	53	53	Ü
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055339	Q94010	Q88271	045633	017756	051275	P97408	Q05787	023097	019891	026562	062239	P74210	008990	051516	013601	061088	000288	043689	000289	043690	Q15982	P76923	044413	COTTOR
SPIKE GLYCOPROTEIN S1	T08G11.1.	NON-STRUCTURAL PROTEIN	K01G12.3.	F01D4.1.	HYPOTHETICAL 39.1 KD P	TYPE II COLLAGEN ANTIB	CHROMOSOME XII COSMID	BAC TM018A10.	F28H7.3.	HYPOTHETICAL 31.5 KD P	F44G3.8.	NITROGEN ASSIMILATION	ADSEVERIN.	HYPOTHETICAL 68.1 KD P	PI006 PROTEIN.	HYPOTHETICAL 42.0 KD P	SINGLE-CHAIN FV FRAGME	ANTI-HER3 SCFV (FRAGME	SINGLE-CHAIN FV FRAGME	ANTI-MPL SCFV (FRAGMEN	RHEUMATOID FACTOR C6 L	SIMILAR TO.	T07A9.2 PROTEIN	CHICINE BETAINE, ETRIC
7.85e+01	5.32e+01	5.32e+01		5.32e+01	5.32e+01	5.32e+01	3.58e+01	3.58e+01	3.58e+01	3.58e+01	2.40e+01	2.40e+01	2.40e+01	2.40e+01	2.40e+01		2.40e+01	2.40e+01	2.40e+01	2.40e+01		1.60e+01	1.60e+01	T. OUETUI

RRR COORDINATE	o p x m o	SON	DIT DAC
ID 063693 PRELIMINARY; PRT; 771 AA. AC 063693; DT 01-NOV-1996 (TREMBLREL. 01, CREATED) DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE) DP HODPHOLIPASE C DELTA4. OS RATTUS NORVEGICUS (RAT). OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; CC EUTHERIA; RODENTIA. RN [1] RP SEQUENCE FROM N.A. RC STRAIN-DONRYU;	Query Match 82.4%; Score 56; DB 1; Length 236; Best Local Similarity 85.7%; Pred. No. 4.58e+00; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Mismatches 1; Mismatches 0; Indels 0; Gaps 0; Matches 1; Mismatches 0; Indels 0; Gaps 0; Mismatches 1; Mismatches 0; Indels 0; Gaps 0; Mismatches 1; Mismatches 0; Indels 0; Mismatches 0; M	ARCHAEBACTERIA; CRENARCHAEOTA; SULFOLOBALES. [1] SEQUENCE FROM N.A. STRAIN=P2; MEDLINE; 97055432. MEDLINE; 97055432. SENSEN C. W., KLENK H.P., SINGH R.K., ALLARD G., CHAN C.C.Y., LIU Q.Y., PENNY S.L., YOUNG F., SCHENK M.E., GAASTERLAND T., DOOLITTLE W.F., PENNY S.L., YOUNG F. B.L.; MOL. MICROBIOL. 22:175-191(1996). EMBL; Y08257; E283822; - PFAM; PF00730; Endonuclease_3. ENDONUCLEASE. SEQUENCE 236 AA; 26843 MW; 31E2C546 CRC32;	RESULT 1 ID 995945 PRELIMINARY; PRT; 236 AA. P95945; O1-MAY-1997 (TREMBLREL. 03, CREATED) DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE) DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE) DE ENDONUCLEASE III. DE ENDONUCLEASE III. DE SULFOLOBUS SOLFATARICUS.

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Qy
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LIU N., FUKAMI R., YU H., TANDAMI,
J. BIOL. CHEM. 271:355-360(1996).

REMBL; D50455; G1304189;
R PFAM; PF00036; efhand.
JR PFAM; PF00186; C2.
DR PFAM; PF00387; PI-PLC-Y.
DR PFAM; PF00388; PI-PLC-Y.
DR PFAM; PF00388; PI-PLC-Y.
DR PFAM; PF00388; PI-PLC-Y.
DR PFAM; PF00387; PI-PLC-Y.
DR PFAM; PF00387; PI-PLC-Y.
DR PFAM; PF00387; PI-PLC-Y.
DR PFAM; PF00387; PI-PLC-Y.
DR PFAM; PF00380; PI-PLC-Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQ SQ
      Query Match
                                                                                                                                                                                                                                                                                                                                  Query Ma
Best Loc
Matches
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE DAWLEY; TISSUE-BRA MEDLINE; 96132878.

LEE S.B., RHEE S.G.;
J. BIOL. CHEM. 271:25-31(1996).

EMBL; U16655; G5711466; -.

PFAM; PF00036; efhand.

PFAM; PF00168; C2.

PFAM; PF00387; PI-PLC-Y.

PFAM; PF00388; PI-PLC-X.

SEQUENCE 772 AA; 88966 MW; 6F
                                                                                                                                                           Q99818 PRELIMINARY; PRT; 108 AA.
Q99818;
Q99818;
Q1-MAX-1997 (TREMBLREL. 03, CREATED)
Q1-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
Q1-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
ANTI-SSDNA ANTIBODY LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                          NON_TER
NON_TER
SEQUENCE
                                                    SUENAGA R.;
SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ
EMBL; U82258; G1773057; -.
PFAM; PF00047; 1g.
                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q62711;
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHOLIPASE C DELTA-4.

RATTUS NORVEGICUS (RAT).

EUKARYOTA: METAZOA; CHORDATA;

EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                            191 DSEEFVQFY 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      062711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 DSEEFVQFY :||:||:|
                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                             ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 55.6%;
                                                                                                                                                                                                                                                                                     ESEDFVAYY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :||:|| :|
ESEDFVAYY 107
                          108 AA;
                                       108
                                                                                                                                                                                                                                                                                                                                82.4%;
llarity 55.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199
                         11792 MW;
  79.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   %
01,
01,
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  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                               Score 56; DB 11;
Pred. No. 4.58e+00;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; DB 11;
Pred. No. 4.58e+00;
3; Mismatches 1
                       876D5BA3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                            6FE7ACA1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F347F051 CRC32;
  54
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 DB
                                                                               DATA
4.
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Length
                                                                               BANKS
                                                                                                                                                                                                                                                                                                                                                     Length 772
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                                                                                                                                                                                                                                                                                                                               Indels
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RESULT 6
ID 014538 PRELIMINARY;
AC 014538;
AC 01-JAN-1998 (TREMBLREL. 05, L#
DT 01-JAN-1998 (TREMBLREL. 07, L#
DT 01-AUG-1998 (TREMBLREL. 07, L#
DE HRV FAB N28-VL (FRAGMENT).
OC EURARYOTA, METAZOA; CHORDATA;
AC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PBL;
RA ITOH K., SUZUKI T.;
RA ITOH K., SUZUKI T.;
RA ITOH K., SUZUKI T.;
AC SUBMITTED (AUG-1997) TO EMBL/G
DR EMBL; AB006845; D1023044; -.
DR PFAM; PF00047; 19.
FT NON_TER 114 AA; 12283 MW;
         RESULT
ID 01
AC 01
DT 01
DT 01
DT 01
DT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT AC OIL AC
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local
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    O14537;
O14537;
O1-JAN-1998
O1-JAN-1998
O1-AUG-1998
HRV FAB N27-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-PBL;
ITOH K., SUZUKI T.;
SUBMITTED (AUG-1997) TO EMB
EMBL; AB006848; D1023046; -
PFAM; PF00047; 19.
NON_TER 113 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           014539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TREMBLREL
01-JAN-1998 (TREMBLREL
01-AUG-1998 (TREMBLREL
HRV FAB 026-VL (FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUTHERIA;
                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                              82
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                                                                                                                                                                                                                ESEDFVAYY 107
                                                                                                                                                                                                                                                           EPEDFAVYY 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESEDFVAYY 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESEDFVAYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 79.4%;
Similarity 66.7%;
6; Conservative
8 (TREMBLREL. 05, 8 (TREMBLREL. 05, 8 (TREMBLREL. 07, 7-VL (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIMATES
                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 AA;
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TO EMBL/GENBANK/DDBJ DATA BANKS
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                                                                                                                                                                                                                                                                                                                                                                                                WW.
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         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                  Score 54; D
Pred. No. 1.
1; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 1.06e+01;
1; Mismatches 2
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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1; }
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                                                                                                                                                                                                                                                                                                                                                                                         BFE57FD0 CRC32;
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                                                                                                                                                                                                                                                                                                    Mismatches
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1.06e+01
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                                                                                                                                                                                                                                                                                               <u>ب</u>
                                                                                                                                                                                                                                                                                                                                             Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 113;
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RESULT RESULT ON ACCORD OF THE SERVICE OF THE SERVI
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Matches
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Best Local
Query Match
Best Local Similarity
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Q13217;
Q13217;
Q13217;
Q13217;
Q1-NOV-1996 (TREMBLREL. 01, CR: 01-NOV-1996 (TREMBLREL. 01, LA: 01-UN-1998 (TREMBLREL. 05, LA: 01-UN-1998 (TREMBLELEL. 05, LA: 01-UN-1998 (TREMBLELEL. 05, LA: 01-UN-1998 (TREMBLEL). 05, LA: 01-UN-1998 (TREMBLEL). 06, LA: 01-UN-1998 (TREMBLEL). 06, LA: 01-UN-1998 (TREMBLEL). 06, LA: 01-UN-1998 (TREMBLEL). 07, LA: 01-UN-1998 (TREMBLEL). 08, LA: 01-UN-1998 (TREMBLEL). 09, LA: 01-UN-1998 (TREMBLEL). 01, LA: 01-UN-1998 (TREMBL
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042983;
01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
HYPOTHETICAL 28.9 KD PROTEIN.
SPBC24E9.03C.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITOH K., SUZUKI T.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; ABO06844; D1023043; -.
PFAM; PF00047; 1g.
NON_TER 115 115
SEQUENCE 115 AA; 12417 MW; 96E3C279 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-PBL
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EMBL; ALOZ1816, E1250650; -
HYPOTHETICAL PROTEIN.
SEQUENCE 251 AA; 28915 MW; 93F693A6 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYNE M., PURNELLE B., BARRELL B.G.;
                                                                                                                                       KORTH M.J., LYONS C.N., WAMBACH M., KATZE M.G.;
GENE 170:181-188(1996).
EMBL; U28424; G1353270; -.
PFAM; PF00226; DnaJ.
PFAM; PF00525; TPR.
SEQUENCE 504 AA; 57580 MW; 86270C88 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 DEFVSYY 241
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Local Similarity 66.7%;
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 ESEDFVAYY 107
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.; 12417 MW;
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     79.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54; DB 3;
Pred. No. 1.06e+01
3; Mismatches
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Pred. No. 1.06e+01
1; Mismatches
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LAST SEQUENCE UPDATE)
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Pred.
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          54; DB 4; L
No. 1.06e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504
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                                             Length 504;
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RESULT 12
ID Q61588
AC Q61588;
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Best Local Similarity
3; Conser
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Best Local
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27968 PRELIMINARY; P. Q27968; P. (TREMBLREL 01, CRE 01-NOV-1996 (TREMBLREL 05, LAS: 01-JUN-1998 (TREMBLREL 06, LAS: PKR INHIBITOR PS B. BOS TAURUS (BOVINE).
BUKARYOTA, METAZOA; CHORDATA; VEUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF TO PRELIMINARY; PRT; 504 AA.

Q60873;

01-NOV-1996 (TREMBLREL. 01, CREATED)

01-NOV-1996 (TREMBLEEL. 06, LAST SEQUENCE UPDATE)

01-JUN-1998 (TREMBLEEL. 06, LAST ANNOTATION UPDATE)

PROTEIN KINASE, INTERFERON INDUCIBLE DOUBLE STRANDED

(PROTEIN KINASE INHIBITOR P58).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00226; DnaJ.
PFAM; PF00515; TPR.
SEQUENCE 504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE; 94187704.

LEE T.G., TANG N., THOMPSON S., MILLER J.,

MOL. CELL. BIOL. 14:2331-2342(1994).

EMBL; U04631; G468012;

PFAM; PF00226; DnaJ.

PFAM; PF00515; TPR.
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EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRKRI
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Similarity 33.3%;
3; Conservative
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                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57704 MW;
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Pred. No. 1
6; Mismat
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LAST SEQUENCE UPDATE)
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Pred. No. 1.06e+(
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No. 1.06e+01;
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01-NOV-1996 (01-JUN-1998 (G8(ANTI-MRBC G8.

5 (TREMBLREL.
3 (TREMBLREL.
3C HYBRIDOMA)

01, LAST SEQUENCE UPDATE)
06, LAST ANNOTATION UPDAT
LIGHT CHAIN.

UPDATE)

MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; EUTHERIA; RODENTIA.

VERTEBRATA;

TETRAPODA; MAMMALIA;

STRAIN-NZB; MEDLINE; 92185208.

SEQUENCE FROM N.A.

Query Match Best Local s Matches

Local Similarity 66.7%; es 6; Conservation

Score 53; DB 11; Pred. No. 1.60e+01; 2; Mismatches 1

Length 81,

Mismatches

Indels

0;

Gaps

0

5AF33092

CRC32;

CAULFIELD M.J., STANKO D.; J. IMMUNOL. 148:2068-2073(1992). EMBL; X60425; E41199; -. PFAM; PF00047; 1g. SEQUENCE 81 AA; 8945 MW; SAF

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AC DT DT DT DT DE DE COC OC OC OC OC OC OC OC OC
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SEQUENCE FROM N.A. MEDLINE; 94033036.
                                                                  RF-V<KAPPA>1.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
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01-NOV-1996 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
RF-V KAPPA 1-RHEUMATOID
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Q16079;
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EMBL; S67060; E99154; -
PFAM; PF00047; 19.
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RF-V<KAPPA>1.

HOMO SAPIENS (HUMAN).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

EUTHERIA; PRIMATES.
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Q16078;
Q16078;
Q16078;
Q16078;
Q1-NOV-1996 (TREMBLREL. 01, CREATED)
Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
Q1-UN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
RF-V KAPPA 1=RHEUMATOID FACTOR V KAPPA REGION (CLONE SLKV7)
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Pred. No. 1.60e+01;
3; Mismatches 1;
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Search completed: Tue Apr Job time : 37 secs.

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HORN M.P., VOGEL M., BIX
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EMBL; Y08148; E274854; -
PFAM; PF00047; 19.
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01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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AUTOIMMUNITY 15:163-170(1993).
EMBL; S67061; E98155; -
PFAM; PF00047; 1g.
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Local Similarity 55.6%;
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MPsrch_pp on: protein - protein database search, using Smith-Waterman algorithm Tue Apr 20 14:08:23 1999; MasPar time 2.95 Seconds

abular output not generated.

Title: Description: Perfect Score: >US-08-836-455-1_1 (89-97) from trans.pep (3 of 3) 54 1 SDYSLTISS 9

Sequence:

Scoring table: PAM 150 Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

pir58 1:pir1 2:pir2 3:pir3 4:pir4

Mean 22.382; Variance 27.684; scale 0.808

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 2 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors	Query Matcl Best Local Matches Db 51 SD Qy 89 SD	5 - 1 - 5 - 5 - 6 - 16 - 17 - 31 - 32 - 38 - 39 - 70 - 71 - 79 - 80 - 88 - 80 - 88 - SUMMARY	##molecu ##rmolecu ##residu CLASSIFICATION KEYWORDS	REFERENCE #authors #journal #title #cross-r	ENTRY TITLE ORGANISM DATE
2 \$17622 #type complete Ig kappa chain V region - mouse SM #formal_name Mus musculus #common_name house mouse 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-May-1997 IONS \$17622 S17625 S17626 Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.	Query Match 100.0%; Score 54; DB 2; Length 88; Best Local Similarity 100.0%; Pred. No. 4.80e-01; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 51 SDYSLTISS 59	#region framework 1\ 6 #region complementarity-determining 1\ 31 #region framework 2\ 38 #region complementarity-determining 2\ 70 #region framework 3\ 79 #region complementarity-determining 3\ 88 #region framework 4 #region framework 4 #region framework 4	molecule_ residues CATION	ERENCE PLO231 ERENCE Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, #authors Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.; Weigert, M. #journal J. Exp. Med. (1990) 171:265-297 #title Anti-DNA antibodies from autoimmune mice arise by clonal #title expansion and somatic mutation. #cross-references MUID:90111618	, L

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#title Anti-DNA antibodies from autoimmune mice
expansion and somatic mutation.
#cross-references MUID:9011618
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##residues 1-91 ##label CLA
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                                                           1-106 ##label SHL
#superfamily immunoglobulin
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If kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
                                                heterotetramer;
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heterotetramer; immunoglobulin
#length 91 #molecular-weight 9895 #checksum 3446
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*superfamily immunoglobulin V region; immunoglobulin
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J. Exp. Med. (1992) 176:761-779
Both IgM and IgG anti-DNA antibodies are the producionally selective B cell stimulation in (NZB x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PH1062 #type fragment
Ig 11ght chain V region (clone 202.105) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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#length 98 #cl
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D.; Marshak-Rothstein, A.; Weigert, M.
#journal J. Exp. Med. (1990) 171:265-297
#title Anti-DNA antibodies from autoimmune mice arise
expansion and somatic mutation.
#cross-references MUID:90111618
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D.; Marshak-Rothstein, A.; Weigert, P.
#journal J. Exp. Med. (1990) 171:265-297
#title Anti-DNA antibodies from autoimmune mic
expansion and somatic mutation.
#cross-references MUID:90111618
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##molecule_type mRNA
##residues 1-106 ##label SHL
IFICATION #superfamily immunoglobulin V region;
RDS heterotetramer; immunoglobulin
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Similarity 100.0%;
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Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
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Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
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#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1160-1165
#title A genetic approach to the generation of antibodies with
enhanced catalytic activities.
#cross-references MUID:93165660
#accession B47271
                                                                            #title Structure and expression of kappa-chain IgE-producing rat immunocytomas. #cross-references MUID:86137406
                                                                     #accession
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framework 3\
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Pred. No. 4.80e-(
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Pred. No. 4.80e-01;
                                                                                                                                                                                                                                                                                                                                                . No. 4.80e-01; Mismatches 0;
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                         immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #journal #title
#authors Burstein, Y.; Schechter, I.
#journal proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720
#title Amino acid sequence of the NH-2-terminal extra piece segments
of the precursors of mouse immunoglobulin lambda-1-type and
kappa-type light chains.
#cross-references MUID:77148916
                                                                                                                                                                                                            #accession
                                                                                                                                                                                                                                                                             #authors Seidman, J.G.; Max, E.E.; Leder, P.
#journal Nature (1979) 280:370-375
#title A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.
#cross-references_MUID:79221900
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#accession D32513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-129 ##label KOF
##cross-references GB:M20832; NID:g196941; PID:g196942
IFICATION #superfamily immunoglobulin V region; immuno
RDS heterotetramer; immunoglobulin
RY #length 129 #molecular-weight 14097 #chec)
                                                                                                                                                                 ##molecule_type DNA
##residues 1-117 ##label VK41
                                                                                                                                                                                                                           ##residues
                                                                                                                                                      ##note
                                                                                                                                                                                                                                       ##molecule_type DNA
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Local Similarity 100.0%;
hes 9; Conservative
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Similarity 100.0%;
9; Conservative
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Ig kappa chain precursor V region (BXW16) - mouse
#formal_name Mus musculus #common_name house mouse
21-May-1990 #sequence_revision 31-Dec-1990 #text_change
20-Mar-1998
D32513
                                                                                                                                                                                                          B93211
                                                                                                                                                                                                                                                                  A9321
                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain precursor V region (MOPC 41) - mouse Ig kappa chain precursor V region VK41 grane Mus musculus #common_name house mouse 24.Apr-1984 #sequence_revision 24-Apr-1984 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin kappa light chain variable region
organization and immunoglobulin genes encoding
autoantibodies in lupus mice.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kofler, R.; Strohal, R.; |
Noonan, D.J.; Duchosal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #length 129
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                                                                                                                               the sequences were determined from the differentiated gene MOPC 41 and the germline gene VK41
                                                                                                                                                                                                                           1-130 ##label PC41
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Pred. No. 4.80e-01;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54; DB 2; L
Pred. No. 4.80e-01;
0; Mismatches 0
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, M.A.; Dixon, F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #checksum 5336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin homology
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.J.; Theofilopoulos
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Mechanism of antibody synthesis:
mouse kappa chains
#cross-references MUID:67056897
#accession A94239
                                                                                                                                                                                                                                    #cross-references MUID:90349634
                                                                                          ##molecule_type protein

##residues 23-49,'8',51-53,'LSB',57-58,'ZZ',61-62,

##residues 78-108,110-130 ##label GRA

78-108,110-130 ##label GRA
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                                 h 92.6%;
Similarity 100.0%;
8; Conservative
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Similarity 100.0%;
9; Conservative
                                                                                                                                                                                                                                        Caton, A.J.; Roprowski, H.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6450-6454
Influenza virus hemagylutinin-specific antibodies isolated
from a combinatorial expression library are closely relat
to the immune response of the donor.
                                                                                                                                                                                                                      A34966
                                                                                                                                                                                                                                                                                                                                                                                A34966 #type fragment
Ig heavy chain V region (PR8-9) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *superfamily immunoglobulin V region; immunoglobulin homology
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Gray, W.R.;
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                                                                                                                                                                                                                                                                                                                                                                      08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin heterotetramer subunit consists of two identical light (Kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                 preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #product Ig kappa chain V region (MOPC 41) #status
experimental #label M41\
#domain immunoglobulin homology #label IMN\
#disulfide_bonds #status predicted
gth 130 #molecular-weight 14311 #checksum 6707
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1-33 ##label BUR
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                               Score 50; DB 2; I
Pred. No. 3.42e+00;
0; Mismatches (
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Pred. No. 4.80e-01;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 8; Conservative
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Best Local
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#accession S13701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors
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##status
                                                                                                                                                                                                                                   ##cross-references EMBL:X53354
FIGATION #superfamily immunoglobulin V region; immunoglobulin homology
UDS heterotetramer; immunoglobulin
4 #length 101 #checksum 6598
                                                                                                                          70 DYSLTISS
                                                                                                                                                                                                                                                                                                            ##residues
                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                               ##status
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                                                                                                          90
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Local Similarity 100.0%;
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C28840 #type fragment
Ig kappa chain V region ()
#formal_name Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                       Pennell, C.A.; Mercolino, T.J.; Grdi:
Haughton, G.; Clarke, S.H.
Eur. J. Immunol. (1989) 19:1289-1295
Biased immunoglobulin variable region
B cells due to clonal selection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Mus musculus #common_name house mouse
21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
09-May-1997
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Ig kappa chain V region
(fragment)
#formal
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Both IgM and IgG anti-DNA antibodies are the clonally selective B cell stimulation in (N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PH1065 *type fragment
Ig kappa chain V region (clone 163.47) - mouse (fragment)
*formal_name Mus musculus *common_name house mouse
30-Sep-1993 *sequence_revision 30-Sep-1993 *text_change
13-Feb-1998
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Pred. No. 3.42e+00;
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38-112 45-110 SUMMARY

Query Match Best Local Matches

FEATURE 1-22

3-22

23-130

CLASSIFICATION KEYWORDS

GENETICS

#introns

products of NZB x NZW)F1

REFERENCE

##note

#authors

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89 91

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Arnold, L.W.;

mouse

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Gaps

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homology

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ACCESSIONS REFERENCE

#journal
#title

#authors

#accession

##status

ORGANISM

CLASSIFICATION KEYWORDS

Query Match Best Local S Matches

musculus

house

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TITLE
ORGANISM
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                        Search completed: Tue Apr 20 14:08:41 1999 Job time: 18 secs.
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Best Local Similarity 100.0%;
Matches 8; Conservative
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#title The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.

#cross-references MUID:86136012

#accession B28840

##molecule_type mRNA

##restainer
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#title The idiotypic network and the internal image: possible regulation of a germ-line network by paucityene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.

#cross-references MUID:86136012

#accession C28840
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##residues 1-101 ##label OLL
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heterotetramer; immunoglobulin
#length 101 #checksum 5983
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#superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin henoth 101 #checksum 7015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B28840 #type fragment
If kappa fanain V region (HP27) - mouse (fragment)
#formal_name Mus muscullus #common_name house mouse
29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change
16-Aug-1996
B28840; I25114
A91028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau,
                                                                                                                                                                            Score 50; DB 2; I
Pred. No. 3.42e+00;
0; Mismatches C
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Tue Apr 20 14:07:20 1999; MasPar time 2.27 Seconds 106.236 Million cell updates/sec

Title: >US-08-836-455-1_1
Description: (89-97) from trans.pep (3 of 3)
Perfect Score: 54
Sequence: 1 SDYSLTISS 9

Scoring table: PAM 150
Gap 11
Searched: 74019 seqs, 2684029

arched: 74019 segs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swissprot

Statistics: Mean 22.743; Variance 22.907; scale 0.993

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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20	45	ω	108	_	KV5T_MOUSE	KAPPA CHAIN
21	45	ω	108	_	KV1H_HUMAN	KAPPA CHAIN V-I
22	45	ω	108	_	KV5R_MOUSE	CHAIN V-V
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ALIGNMENTS

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MEDLINE; 82150934.
SIEGELMAN M., CAPRA J.D.;
PROC. NATL. ACAD. SCI. U.S.A.
-i- ANTI-ARSONATE HYBRIDOMA PI
PIR; A01927; KVMSAR.
HSSP; P01607; 1FAI.
                                                                                                                                                                                                                                                                                                   PO1644;
21-UIL-1986 (REL. 01, CREATED)
21-UIL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-UIL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-V REGION (HP R16.7).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMUNOGLOBULIN V REGION; SIGNAL. SIGNAL 1 20
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HSSP; P01607; 1IIF.
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MEDLINE; 81220975.
MEDLINE; 81220975.
PECH M., HOCHTL J., SCHNE
PATURE 291:668-670(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-CCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN PRECURSOR V-V REGION (L6) (FRAGMENT).
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Local Similarity 100.0%;
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                                                                                                                        ANTIARSONATE ANTIBODY.
FRAMEWORK 1.
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0; Misma
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 3.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 3.

COMPLEMENTARITY-DETERMINING
BY SIMILARITY.
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STRAIN-A/J;
MEDLINE; 82150934.
SIEGELMAN M., CAPRA J.D.;
PROC. NATL. ACAD. SCI. U.S.A.
-!- ANTI-ARSONATE HYBRIDOMA PI
PIR; A01927; KYMSAR.
HSSP; P01607; 1FAI.
IMMUNOGLOBULIN V REGION; ANTI.
DOMAIN
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P01647;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQU
01-OCT-1993 (REL. 27, LAST ANNO
IG KAPPA CHAIN V-V REGION (HP 1
MUS MUSCULUS (MOUSE).
EUKARYOTA, METAAOA; CHORDATA; V
EUTHERIA; RODENTIA.
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                                                                                                                                                       SEQUENCE
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DOMAIN
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN Y-V REGION (MOPC 173).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                        EUR. J. BIOCHEM. 59:525-537(1975).
-I- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN PIR; A01926; KYMS73.
HSSB; P01607; 1FAI.
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P01643;
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                                                                     1. 78:7679-7683(1981). PROTEIN.
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Pred. No.
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Pred. No. 8.08e-01
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.

BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.
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21-JUL-1986 (REL. 0
21-JUL-1986 (REL. 0
01-OCT-1993 (REL. 2
                                                                    IG KAPPA CHAIN V-V RE MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CEUTHERIA; RODENTIA.
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MEDLINE; 82150934.
SIEGELMAN M., CAPF
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21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT 1993 (REL. 27, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN V-V REGION (HP 91A3).
IG KAPPA CHAIN V-V REGION (HP 91A3).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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HSSP; P01607; 1FAI.
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                   STRAIN-A/J;
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77.8%;
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FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3
FRAMEWORK 4.
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Pred. No.
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MEDLINE; 82150934.
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EUKARYOTA; METAZOA; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UP
01-CTT-193 (REL. 27, LAST ANNOTATION
IG KAPPA CHAIN V-V REGION (HP 123E6).
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HSSP; P01607; 1FAI.
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PROC. NATL. ACAD. SCI. U.S.A. 78:767
-1- ANTI-ARSONATE HYBRIDOMA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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69 TDYSLTISN 77
:||||||:
89 SDYSLTISS 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MMUNOGLOBULIN V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 SDYSLTISS
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                                                                                                                                     Similarity
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                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAPRA J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAPRA J.D.;
CAD. SCI. U.S.A. 78:7679-7683(1981).
                                                                                                                                                                                                                   Ä,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGION;
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                                                                                                                                  90.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTIARSONATE ANTIBODY.
FRAMEWORK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTIARSONATE ANTIBODY.
                                                                                                                                                                                                                   MW;
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A PROTEIN.
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Pred. No.
                                                                                                                                  Score 49; DB 1;
Pred. No. 8.08e-01
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COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
                                                                                                                                                                                                                                                                  FRAMEWORK 3.

COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                   23B8BB67 CRC32;
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                                                                                                            Mismatches
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No. 8.08e-01;
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                                                                                                                                                              Length 108;
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Best Local Similarity
Matches 6; Conse
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE NO.
STRAIN-BRISTOL N2:
STRAIN-BRISTOL N2:
DU Z., WATERSTON R.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
EMBL: UJ3453; G73576; --
WORMPEP: B0252.3; CE02419.
HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMUNOGLOBULIN V REGION; H

DOMAIN

DO
                                                                                TCPH_SCHPO
P87153;
15-JUL-1998
15-JUL-1998
15-JUL-1998
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Q10917;
Q1-0CT-1996
Q1-0CT-1996
Q1-0CT-1996
                                                          15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PROBABLE T-COMPLEX PROTEIN 1, ETA SUBUNIT (TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- ANTI-2-PHENYL OXAZOLONE (PHOX)
EMBL; K00745; G196455; -.
HSSP; P01607; 1FAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F., NATURE 304:320-324(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 83271467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                        / Match 87.0%;
Local Similarity 87.5%;
les 7; Conservative
                                                                                                                                                                                                                                                                             90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 TDYSLTITN 77
                                                                                                                                                                                                                                                                                                                         13 DYNLTISS 20
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                                       OR SPBC25H2
                                                                                                                                                                                                                                                                             DYSLTISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REL. 34, CREATED)
(REL. 34, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDAT
48.6 KD PROTEIN B0252.3 IN CHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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TES POMBE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WW;
                 (FISSION YEAST)
                                                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 1; I
Pred. No. 2.47e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 1; I
Pred. No. 2.47e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAMEWORK 2.
                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D396F142 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                             558 AA
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                                                             (TCP-1-ETA) (CCT-ETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MILSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 435;
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                         Query Match
Best Local S
Matches
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Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                                                                       KV6C_MOUSE STANDARD;
P01677;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUI
01-OCT-1993 (REL. 27, LAST ANNO:
IG KAPPA CHAIN V-VI REGION (TEPO
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VI
                                                                                                                                                                                               SEQUENCE (TEPC 191).

MEDLINE; 81054757.

RUDIKOFF S., RAO D.N., G
PROC. NATL ACAD. SCI. U
PROT. THE TWO SEQUENCES AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS
PROSITE; PS
CHAPERONE;
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STRAIN-972;
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                                                                                                                                          DOMAIN
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HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                            SEQUENCE (TEPC 601).
MEDLINE; 79082830.
RAO D.N., RUDIKOFF S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                 EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
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[1]
                                                                                        DOMAIN
                                                                                                                                    MIAMOC
                                                                                                                                                                                                                                                    BIOCHEMISTRY 17:5555-5559(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DURSO G.,
                                                                                                                                                                                       - ! - THESE CHAINS WERE
                                                                                                                                                      MMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                        427 DYSLTISG
                         Local Similarity hes 7; Conser
68 TSYSLTISS 76
                                                                                                                                                                                                                                                                                                                                                                                                         90
                                                                                                                                                                               GALACTAN.
                                                                                                                                                                                                                                                                                                                                                                                                        DYSLTISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 295397; E315886; -.
ITE; PS00750; TCP1_1; 1.
ITE; PS00751; TCP1_2; 1.
ITE; PS00995; TCP1_3; 1.
ERONE; ATP-BINDING; MULTIC
ENCE 558 AA; 60686 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYE G.,
                                                                                                                                                                                                                                                                                                 RODENTIA.
                                                             107
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         434
                                                             AA;
                                                                      REGION
23
33
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106
106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOWMAN S.,
                                   85.2%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.0%;
87.5%;
                                                                                                                                                                                                                                                                                                        CHORDATA; VERTEBRATA;
                                                             11568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60686 MW;
                                                                                                                                                                                                ARE IDENTICAL
                                                                                                                                                                                       ISOLATED
                                                                                                                                                                                                        GLAUDEMANS C.P.J., POTTER U.S.A. 77:4270-4274(1980).
                                                                                                                                                                                                                                                             POTTER M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MULTIGENE FAMILY.
                                                             MW.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE UPDATE)
ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                          (TEPC 601 AND TEPC
                        Score 46;
Pred. No.
1; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                              COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
BY SIMILARITY.
                                                                                                         COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
                                                                                                                          FRAMEWORK
                                                                                                                                   COMPLEMENTARITY-DETERMINING
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                                                                                                                                            FRAMEWORK 1.
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                                                             154F6572 CRC32;
                                                                                                                                                                                       FROM MYELOMA PROTEINS THAT BIND
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                           Mismatches
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No. 2.47e+00;
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                                   DB 1; L
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                                          Length 107;
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                           Indels
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SDYSLTISS

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KV6D_MOUSE P01678;

STANDARD;

PRT;

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Best Local Similarity
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SEQUENCE
                                         NON_TER
SEQUENCE
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21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-OCT-1983 (REL. 27, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN V-VI REGION (XRPC 44).
MUS MUSCULUS (MOUSE).
EUKARYCTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUI-1986 (REL. 01, CREATED)
21-JUI-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN V-VI REGION (SAPC 10).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                 MEDLINE; 79082830.

RAO D.N., RUDIKOFF S., POTTER M.;
BIOCHEMISTRY 17:5555-5559(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KV6A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 81054757.
RUDIKOFF S., RAO D
PROC. NATL. ACAD.
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HSSP; P01679; 2FBJ.
                                                                                DISULFID
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HSSP; P01679; 2FBJ.
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                                           MW;
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Pred. No. 4.26e+00
  Score
                                                                                FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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Length 107;
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Best Local s
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                       107 AA.

108 (REL. 01, CREATED)

21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

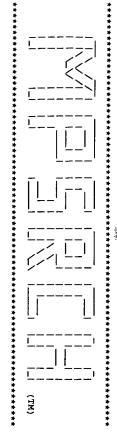
11-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)

12 KAPPA CHAIN Y-VI REGION (XRPC 24).

MUS MUSCULUS (MOUSE).

EUKARYOTA; METAZOA. COCC.
time : 5 secs.
                                                                                                          DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                                             -!- THIS CHAIN WAS IS
PIR; A01941; KVMSX4.
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                        RAO D.N., RUDIKOFF S., POTTER M.;
BIOCHEMISTRY 17:5555-5559(1978).
                                                                                                                                                                                                                                                          SEQUENCE.
MEDLINE; 79082830.
                                                                                                                                                                                                                                                                                     EUTHERIA;
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                                    89 SDYSLTISS
                                                    68 TSYSLTISS 76
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                                                                                85.2%;
77.8%;
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                                                                                                            11584 MW;
        20 14:07:25
                                                                               Score 46; DB 1; 1
Pred. No. 4.26e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 4.26e+00;
1; Mismatches 1;
                                                                                                                              ВΥ
                                                                                                                                      COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
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                                                                                                                                                                                   COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                            FRAMEWORK 1
                                                                                                            91B2CD6E CRC32;
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         1999
                                                                       Mismatches
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

bular output not generated. on: Tue Apr 20 14:07:44 1999; MasPar time 4.19 Seconds """ 106.989 Million cell updates/sec

Description: Perfect Score: Sequence: Title: >US-08-836-455-1_1 (89-97) from trans.pep (3 of 3) 54 1 SDYSLTISS 9

Scoring table: PAM 150 Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_bhage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 21.822; Variance 24.944; scale 0.875

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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14 81.	45 83.	45 83.		45 83.	45 83.		83	83	45 83.	83	83	83	83	83		88	50 92.	92	92	Query re Match
5 94	3 925	3 381	3 244	3 244	3 240										2 787	9 1197		6 107	6 99	y h Length
۰ 4	4	Ç	4	4	4	4	4	4	4	4	4	4	4	4	<u>د.</u>	13	4	11	11	BB
Q16079	060308	016768	043689	000288	000289	043690	Q15986	Q99826	014535	014540	Q99953	099514	Q16078	Q16077	058025	290478	015358	035538	P97409	ID
							-	:												
RF-V KAPPA 1-RHEUMATOI	KIAA0562 PROTEIN	R07C3.8 PROTEIN.	ANTI-HER3 SCFV (FRAGME	SINGLE-CHAIN FV FRAGME	SINGLE-CHAIN FV FRAGME	ANTI-MPL SCFV (FRAGMEN	RHEUMATOID FACTOR D5 L	$\overline{}$	HRV FAB N6-VL (FRAGMEN	HRV FAB 027-VL (FRAGME	VASOACTIVE INTESTINAL	LIGHT CHAIN FAB FRAGME	RF-V KAPPA 1-RHEUMATOI	RHEUMATOID FACTOR KAPP	787AA LONG HYPOTHETICA	ADHESION MOLECULE L1.1	IMMUNOGLOBULIN VARIABL	KAPPA (FRAGMENT).	TYPE II COLLAGEN ANTI-	Description
3.31e+01	2 046+01	2.04e+01	2.04e+01	2.04e+01	2.04e+01	2.04e+01	2.04e+01	2.04e+01	2.04e+01	2.04e+01	2.04e+01	2.04e+01	2.04e+01	2.04e+01	1.25e+01	4.54e+00	1.61e+00	1.61e+00	1.61e+00	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
42	42	42	42	42	42	42	42	42	42	42	42	43	43	43	43	43	43	43	43	43	44	44	44	44
77.8	٠	٠	•	•	77.8				•		•	•	•	•	•	79.6	•		•	•	•	•		•
6642	6632	2335	1232	620	618	470	414	341	248	186	133	2971	974	520	359	346	327	243	132	127	300	291	116	108
σ	u	w	13	N	თ	տ	14	G	11	N	H	œ	N	N	N	N	N	1	ഗ	11	<u>.</u>	<u>, , , , , , , , , , , , , , , , , , , </u>	4	4
001761	Q17362	014356	Q90284	P77890	018693	7	055752	~	Q63818	025653	Q61551	Q32065	991800	Q47163	068206	051194	050299	035140	Q21727	Q61251	058635	059489	Q15982	Q99818
C. ELEGANS UNC-89 (GB:	UNC-89.	PUTATIVE PHOSPHATIDYLI	L1-LIKE CELL ADHESION	RNA POLYMERASE SIGMA F	F28F8.2.	R07C3.3 PROTEIN.	HYPOTHETICAL 49.5 KD P	Y45F10B.6.	IMMUNOTOXIN MIK-BETA 1	CIFIC RECOMBI	CC49 FAB PRECURSOR (FR	SE	CELLULASE 1 PRECURSOR	(CTR5X).	E: (GLUCOS	40.3 KD	8.0 KD	ANTI-CD30 MOAB KI-4 SC	COSMID RO4E5.	ANTIGEN, B-CELL RECEPT	300AA LONG HYPOTHETICA	291AA LONG HYPOTHETICA	RHEUMATOID FACTOR C6 L	ANTI-SSDNA ANTIBODY LI
	8.53e+01	8.53e+01	٠		8.53e+01	٠					8.53e+01	٠			•	5.34e+01		•	•			3.31e+01		3.31e+01

ALIGNMENTS

RESULT ID P97409; AC P97409; DT 01-MAY-1997 (TREMBLREL. 03, CREATED) DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE) DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE) DT 01-MAY-1997 (TREMBLREL. 06, LAST ANNOTATION UPDATE) DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE) DE KAPPA (FRAGMENT). CC EUTHERTA; MOTAZOA; CHORDATA; VERTEBRATA; TETRAPODA; I CC EUTHERTA; MOTAZOA; CHORDATA; VERTEBRATA; TETRAPODA; I

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ID 3538
AC 015358
AC 015358
DT 01-JAN-1
DT 01-JAN-1
DT 01-JAN-1
DT 01-JAN-1
DT 01-JAN-1
DT 01-JAN-1
DE IMMUNOGL
GN VKLA.
OS HOMO SAP
OC EUKARYOT
OC EUTHERIA
RN [1]
RP SEQUENCE
RC TISSUB-BR
RD JULL L.
RL SUBMITTE
RL SUBMITTE
BR SEQUENCE
RA JULL L.
RL SUBMITTE
RA SUBMITTE
RON_TER
SO SEQUENCE
                                       RESULT 4
ID 90478
AC 990478
AC 990478
DT 01-NOV-1
DT 01-NOV-1
DT 01-JUN-1
DE ADHESION
OS BRACHYDD
OC EUKARYOT
OC OSTEICHT
RN [1]
RP SEQUENCE
RX MEDLINE;
RX MEDLINE;
RX TONGLORG
RL J. NEURO
DR EMBL; X8
DR PFAM; PF
DR PFAM; PF
TONO_TER
SQ SEQUENCE
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Best Local S
Matches
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Query Match
Best Local :
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J. FERMENT. BIOENG. 83:333-340(1997).

EMBL; D55701; D1024447; -.

EMBL; D86361; D1024550; -.

PFAM; PF00047; 1g.

NON_TER 107 107

SEQUENCE 107 AA; 11933 MW; 3BF775AC CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998
01-JAN-1998
01-AUG-1998
                                                                                                                                                                                 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
ADHESION MOLECULE L1.1 (FRAGMENT)
BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; G
OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JUUL L., HOUGS L., BARINGTON T.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Y14865; E1169998; -.
PFAM; PF00047; 1g.
NON_TER 17 117
SEQUENCE 117 AA; 12748 MW; 034081EF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKLA.
HOMO SAPIENS (HUMAN).
CHORDATA;
                                                                 TONGIORGI E., BERNHARDT R.R., SCHACHNER M.;
J. NEUROSCI. RES. 42:547-561(1995).
EMBL; X89204; G1065714; -.
PFAM; PF00041; fn3.
PFAM; PF00047; ig.
                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 96155762.
                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMUNOGLOBULIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-BALB/C;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 DYSLTISS 77
                                                                                                                                                                                                                                                                                                                                                     SDYSLTISS
 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 92.6%;
Similarity 100.0%;
8; Conservative
                                    1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G (TREMBLREL.
G (TREMBLREL.
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                         97
                                          AA;
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 88.9%;
                                            132860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05, CREATED)
05, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
REGION, KAPPA LIGHT CHAIN (FRAGMENT).
                                          MW;
Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB 4; 1
Pred. No. 1.61e+00;
2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
0; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERTEBRÄTÄ; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3BF775AC CRC32;
                                          6D9423C0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e 50; DB 11; L
. No. 1.61e+00;
Mismatches 0;
                                                                                                                                                                                                                                                                                                   1197
DB 13;
4.54e+00;
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              Length 1197;
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RESULT 5

PAC 058025;
DT 01-AUG-1998 (
DE 787AA LONG HY
GN PHBM045.
OS PYROCOCCUS HO
OC ARCHAEA; EURY
RN [1]
RP SEQUENCE FROM
RC STRAIN-073;
RA YAMAMOTO S.,
RA YAMAMOTO S.,
RA SAKAI M., OGU
RA FUNAHASHI T.,
RA AOKI K., YOSE
RL SUBMITTED (DE
DR EMBL; AB0094;
SQ SEQUENCE 7;
RESULT 7
ID Q16078
AC Q16078;
DT 01-NOV-1996
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                                                                                                                     Query Match
Best Local S
Matches
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Best Local Similarity
Matches 7; Conser
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                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE; 94033036.

MARTIN T., CROUZIER R., BLAISON
AUTOIMMUNITY 15:163-170(1993).

EMBL; S67059; E98153; -.

PFAM; PF00047; 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAMARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y., YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y., SAKAI M., OGURA K., OTSUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y., FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI AOKI K., YOSHIZAWA T., NAKAMURA Y., MASUCHI Y., SHIZUYA H., KIKUCHI SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; ABO09473; D1027408; -.

SEQUENCE 787 AA; 86903 MW; B47F09A6 CRC32;
                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYROCOCCUS HORIKOSHII. ARCHAEA; EURYARCHAEOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                      54 TDFTLTISS
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                                                                       SDYSLTISS
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                                                                                                                     6; Conser
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98 (TREMBLREL.
98 (TREMBLREL.
3 HYPOTHETICAL
  (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.2%;
larity 100.0%;
Conservative
                                                                                                                      83.3%;
larity 66.7%;
Conservative
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                          PRELIMINARY;
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                                                                         97
                                                                                               62
                                                                                                                                                                       10082 MW;
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01, LAST SEQUENCE UPDATE)
06, LAST ANNOTATION UPDATE)
CHAIN VJ REGION (FRAGMENT).
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07, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDAT
PROTEIN.
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  01,
                                                                                                                                                                                                                                            BLAISON
                                                                                                                     Score 45;
Pred. No.
3; Misma
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Pred. No.
0; Misma
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Mismatches
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                                                                                                                                 DB 4; Lt
2.04e+01;
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1.25e+01;
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                                                                                                                                                                                                                                                                                                      TETRAPODA;
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                                                                                                                                              Length
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                                                                                                                                              93;
                                                                                                                                                                                                                                                                                                      MAMMALIA;
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KIKUCHI H.;
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT IN ACCOUNTS OF THE PROPERTY OF THE PROP
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Best Local S
Matches
                                                                                                                                                                         Q99953 PRELIMINARY; PRT;
Q99953;
Q1-MAY-1997 (TREMBLREL 03, CREATED
Q1-MAY-1997 (TREMBLREL 06, LAST SE)
Q1-JUN-1998 (TREMBLREL 06, LAST AN)
VASOACTIVE INTESTINAL POLYPEPTIDE HI
(FRAGMENT).
MEDLINE: 96375171.
TYUTYULKOVA S., GAO Q.S., THOMPSON A., RENNARD BIOCHIM. BIOPHYS. ACTA 1316:217-223(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
HORN M.P., VOGEL M., BIAGGI C., MIESCHER S
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ
EMBL; Y08148; E274854; -.
PFAM; PF00047; 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q99514
Q99514;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MARTIN T., CROUZIER R., BLAISOI
AUTOIMMUNITY 15:163-170(1993)
EMBL; S67060; E98154; -
PFAM: PF00047; 19
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                               SEQUENCE
                                                                                                                     EUTHERIA; PRIMATES
                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDAT
LIGHT CHAIN FAB FRAGMENT (FRAGMENT).
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01-JUN-1998 (TREMBLREL.
RF-V KAPPA 1-RHEUMATOID
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Local Similarity
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105 AA;
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93
10178 MW;
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06, LAST
FACTOR V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; Di
Pred. No. 2.0
3; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45;
Pred. No.
                                                                                                                                                                                           CREATED)
LAST SOUTENCE UPDATE)
LAST ANNOTATION UPDATE)
EPTIDE HYDROLYZING AUTOANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                     VERTEBRATA;
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ANNOTATION UPDATE)
KAPPA REGION (CLONE SLKV7)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
2.04e+01
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2.04e+01
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                                                                                                                                       TETRAPODA;
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BANKS.
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                                         PAUL
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                                                                                                                                       MAMMALIA
                                                                                                                                                                                               LIGHT
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SDYSLTISS

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RESULT ACCOLUTE ACCOL
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EMBL; AB006842; D1023041; •
PFAM; PF00047; 19:
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SEQUENCE 113 AA; 12207 N
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01-JAN-1998 (TREMBLREL 05,
01-JAG-1998 (TREMBLREL 07,
01-AUG-1998 (TREMBLREL 07,
HRY FAB 027-VL [FRAGMENT)).
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01-JAN-1998 (TREMBLREL 05
01-AUG-1998 (TREMBLREL 07
HRV FAB N6-VL (FRAGMENT).
HGMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDA:
EUTHERIA; PRIMATES.
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SUBMITTED (AUG-1997) TO EMI
EMEL; AB006849; D1023047;
PFAM; PF00047; 19.
NON_TER 113 113
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PFAM; PF00047;
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NON_TER 107
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EUKARYOTA; METAZOA;
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                                                                                                                                                                                                         TOH K.,
                                                                                                                                                                                                                                          EQUENCE FROM N.A.
                                                                                                                                                                                                                         (SSUE-PBL)
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107 AA;
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llarity 66.7%;
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larity 66.7%;
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Pred. No.
3; Misma
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Pred. No. 2.04e+01
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Pred. No. 2.04e+01
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Best Local S
Matches
                                                                                O43690 PRELIMINARY; PRT; 239 AA.
O43590; OF TREMBLEL OF CREATED; O1-JUN-1998 (TREMBLEL OF LAST SEQUENCE UP O1-JUN-1998 (TREMBLEL OF LAST ANNOTATION ANTI-MPL SCFV (FRAGMENT).
HOMO SAPIENS (HUMAN)
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TE
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Q15986;
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Q99826
Q99826;
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EMBL; S56199; G298553; -.
PFAM; PF00047; ig.
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NON_TER
SEQUENCE
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01-NOV-1996 (TREMBLREL. 01,
01-JUN-1998 (TREMBLREL. 06,
RHEUMATOID FACTOR D5 LIGHT C
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-UN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
ANTI-HIV-1 GP120 V3 LOOP ANTIBODY DO142-10 LIGHT CHAIN VARIABLE REGION
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                              EUTHERIA; PRIMATES
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89 SDYSLTISS 97
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Similarity 66.7%;
6; Conservative
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118 AA;
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115 AA;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 4; Leg
Pred. No. 2.04e+01;
3; Mismatches 0;
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Pred. No. 2.04e+01;
3; Mismatches (
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ANNOTATION UPDATE)
(FRAGMENT).
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                                                                                              TETRAPODA; MAMMALIA;
                                                                                                                                                                                                UPDATE)
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Best Local Similarity 66.7%;
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SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF048775; G2911502; -.
NON_TER 1 1
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SEQUENCE 239 AA; 25262 MW; 5B9ABF4C CRC32;
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NAT. BIOTECHNOL. 15:629-631(1997).
EMBL; V13056; E315281; -.
PFAM: PF00047; 1g.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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ALIGNMENTS

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PN W09527045-A1.

PP 12-OCT-1995.

PF 30-MAR-1994; W03420.

PR (IGEN-) IGEN INC.

PR (IGEN-) IGEN INC.

PR (Algen-) Darsley MJ, Fitzgerald K, Kenten JH;

PR MARTIN MT, McCafferty J, Smith RG, Titmas RC, Williams RO;

PR WPI; 95-358624/46.

PR N-PSDB; T04655.

PR N-PSDB; T04655.

PR N-PSDB; T04655.

PT generating a gene library of antibody-derived domains and expressing tit in phage vectors tit in phage vectors

PT generating a gene library of antibody-derived mains and expressing tit in phage vectors

PT generating a gene library of antibody-derived mains and expressing tit in phage vectors

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R80078;
R80078;
22-MAY-1996 (first entry)
Mouse derived light chain RT3 phage antibody pattern A.
Light chain; RT3; murine; catalytic antibody; bacteriophage;
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Sequence

Query Match

Matches

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(LOSW-11 D, Darsley MJ, F
Chiswell D, McCafferty J, S
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Disclosure; Fig 9; 133pp; English.
Disclosure; Fig 9; 133pp; English.
T04626 encodes R80079 mouse derived light chain RT3 phage
The DNA was used in the prepn. of catalytic antibody (CA)
bacteriophage. The CAs can be used to activate/deactivate
biological function in an animal by enhancing the rate of
or formation of a specific bond within a mol. in vivo.
Sequence 90 AA;
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R80079 standard; Protein;
R80079;
    antibody engineering.
Mus musculus.
Locat
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Production of catalytic antibodies displayed on phage -
generating a gene library of antibody-derived domains an
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12-OCT-1995.
30-MAR-1994; U03420
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Mouse derived light chain RT3 phage antibody pattern
Mouse derived light chain RT3 phage antibody; bacteri
                                              Mouse anti-VLA-4 antibody 21.6 light cl
Humanized antibody; leukocyte adhesion
                                                                           02-APR-1996 (first entry)
                                                                                                      R81328 standard; Protein; 106 AA.
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d. No. 1.47e+03;
Mismatches 0;
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                                                                                                                                                                                                               CC variable region (without signal sequence). Cloned cDNA CDR sequences of constant framework regions of the REI antibody for the light chain and ct the 2*CL antibody for the heavy chain in the construction of a humanized constitution of a humanized constant framework regions of the REI antibody for the heavy chain in the construction of a humanized contibody against VIA-4. The 5' and 3' ends of the mouse cDNAs are condified using PCR primers (See Q99895-98) and then subcloned into manufalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, CL58 and L69 in the human kappa LCVR framework are replaced by the amino cald present in the equivalent position of the mouse 21.6 Ig light chain. CC Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VIA-4, for affinity purification or for generating canti-idiotype antibodies.
                                                                                                                                                          Query Match
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w27121 standard; Protein; 107 AA.
w27121;
04-JAN-1998 (first entry)
Murine antibody light chain variable region
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25-JAN 1994; US-186269.
(ATHE-) ATHENA NEUROSCIENCES
Bendig_MM, Jones TS, Leger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory disease.
Disclosure; Page 66; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New humanised antibodies against VLA-4 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9519790-A1.
27-JUL-1995.
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Local Similarity 100.0%;
es 5; Conservation
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/label=
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/note= "mouse light
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lc. for treating
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19-DEC-1996;
13-DEC-1996;
20-DEC-1995;
26-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             especially breast cancer

Example 2: Fig 26c; 130pp: English.

This polypeptide sequence comprises a consensus sequence of murine light chain variable regions (VL) selected on the basis of identity to the VL region (see W27119) of monoclonal anti-idiotype antibody 11D10. The sequences were obtained from a GenBank database search. A VH consensus (W27122) was also produced. 11D10 has at least 18 departures from the consensus sequences (7 in the light chain and 11 in the heavy chain). 8 Occur within CDRs and 10 outside CDRs. 11D10 polypeptides and polynucleotides can be used in vaccines and pharmaceutical compositions for the treatment of human milk fat globule-associated diseases such as breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal
human milk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KENT ) UNIV KENTUCKY Chatterjee M, Chatter 97-341690/31.
                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-1993 (first entry)
WNI 222-5 antibody Light chain Variable domain.
MONOClonal antibody; MAD; epitope; core region;
Lipopolysaccharide; endotoxaemia; WNI 222-5; WNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R27499 standard; Protein; 107 AA. R27499;
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Similarity 100.0%;
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US-575762.
US-575762.
US-591965.
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/note- "complementarity
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24..34
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HMFG; tumour; breast cancer; vaccine.
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Monoclonal antibodies which recognise an epitope in the core region of the bacterial lipopolysaccharide (LPS) mol. and which are crossofthe bacterial lipopolysaccharide (LPS) mol. and which are crossofthe bacterial strains having different core structures, pref. comprise the heavy chain variable domain having the sequence of R27497 (WNI 222-5) or R27500 (WNI 58-9).
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22-FEB-1992; E00380.
13-MAR-1991; GB-005292.
(SANO ) SANDOZ LITD.
(SANO ) SANDOZ PATENT GMBH.
(SANO ) SANDOZ PATENT GMBH.
BAICLAY GR, DI PAGOVA F, Grau
WPI; 92-149209/42.
N-PSDB; 029150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH) GENENTECH INC.

Carter PJ, Presta LG;

WPI; 93-018139/02.

Humanisation of antibodies - by molecular modelling of t domains and alteration by gene conversion mutagenesis Disclosure; Fig 5; 126pp; English.

The sequence is that of the light chain variable domain anti-CD3 monoclonal antibody UCHT1 (muxCD3, Shalaby 1992 Sequence 107 AA;
                       Mus sp.
W09715326-A1.
                                                                                              Anti-human Fasi antibody (NOK1) light chain variable regio Light chain; variable region; mouse; murine; human; Fas li Light chain; variable region; mouse; murine; human; Fas li Fasi, monoclonal antibody; MAb; hybridoma; treatment; hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1992.
15-JUN-1992; U05126.
14-JUN-1991; US-715272.
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Murine anti-CD3 MAD UCHT1 light
Humanisation; rapid; monoclonal
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                                                                       liver cell; glutamate oxaloacetate;
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llarity 100.0%;
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                                                                                                                                                                                                                                                       Protein; 108
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Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB 6; Lei
Pred. No. 1.47e+03;
0; Mismatches 0;
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antibody; muxCD3.
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1. No. 1.47e+03;
Mismatches 0;
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                                                                                                                      hepatitis;
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Claim 6; Pages 30-31; Slpp; Japanese.

The present sequence is the light chain variable region of the murine anti-human Fas ligand (Fast) monoclonal antibody (MAb) NOKI, which is expressed by the hybridoma NOKI (FERM BP-5044). The MAb can be used in the preparation of a composition for the effective oral or parenteral treatment of hepatitis, including hepatitis caused by hepatitis B or C virus. The composition controls apoptosis in liver cells caused by the binding of Fast to Fas expressing liver cells, and improves liver function by improving blood glutamate oxaloacetate and pyruvate transaminase levels. The composition is given in a dosage of 0.0001-1000, preferably 0.01-600 mg/day. Spleen cells from mice immunised with Fast expressing COS cells were fused with mouse myeloma cells to produce hybridomas. The composition of the active clones NOKI-5 isolated.
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                                                                            12-SEP-1994; 010858.
12-SEP-1994; FR-010858.
(INRM ) INSERM INST NAT SANTE & RECH
(PROT-) PROTEINE PERFORMANCE SA
                                                 Bernard A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   region
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27-OCT-1995; JP-303
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Local Similarity 100.0%;
es 5; Conservation
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96-162083/17
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                                                       Cervoni MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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57
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95..10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "complementarity determining region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "framework region"
                                                                                                                                                                                                                                                                                                                                    /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                            'note-
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                                                                                                                                                                                                                                                                                                                                                                                      "framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR1
                                                    Lefranc MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 25;
Pred. No. 1.47e+03;
0; Mismatches 0
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ج. الآر
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display package.

Example 21; Fig 24; 209pp; English.

Example 21; Fig 24; 209pp; English.

The VK sequence is one of seven (R21286-92) found to be expressed from a single chain Fv library from an immunised mouse. The library from a single chain Fv library from an immunised mouse. The library ry produces a diverse repertoire of antibody fragments specific for 2-phenyl-5-oxazolone (phox). It was prepd. using cDNA generated from mRNA from mice immunised with phox coupled to chicked serum albumin. The VH and VL kappa sequences were separately amplified by PCR (see 023470-84) and ligated into fdCAT2 (see 023463) for expression on the phage surface as fusions with gene III. The resulting library of clones was diverse. Twenty three hapten binding clones were sequenced revealing eight different VR genes (A-H) (see R21264-71) in a variety of pairings with the seven different VR genes (a-g). Of the twenty three clones sequenced, three were of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             10-JUL-1990; GB-015198.

19-0CT-1990; GB-022845.

12-NOV-1990; GB-024503.

06-MAR-1991; GB-004744.

15-MAY-1991; GB-010549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-1992.
10-JUL-1991;
10-JUL-1990;
19-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine VI kappa group V chain "a", specific for phox.

Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus; g3p; binding; adsorption; gene VIII; diverse repertoire; specific binding pairs; replicable genetic display package.
                                                                                                                                                                                                                                                              Producing members of specific binding pairs · by expression recombinant host cells with a secreting replicable genetic
                                                                                                                                                                                                                                                                                                  Winter GP, Bonnert TP; WPI; 92-056862/07.
                                                                                                                                                                                                                                                                                                                               (CAMB-) CAMBRILLO.

(MEDI-) MED RES COUNCIL.

Teferty J, Pope AR, Johnson

Teferty J, Pope AR, Marks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of the variable region of the kappa light chain from murine monoclonal antibody K20. The antibody recognises the beta 1 subunit (CD29) of integrins and inhibits activation and proliferation of peripheral T cells induced by anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target for humanisation; the humanisation may be useful as an immunosuppressant. In the humanisation process, the complementarity determining regions (CDRs) of a human antibody with framework regions 70-95% homologous to those of K20 were replaced by the K20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binding_site
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Humanisation of non-human immunoglobulin variable regions -
prodn. of humanised antibodies, esp. K20, e.g. as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-1992 (first entry)
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/note="
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D-X-G-X-X motif "
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Pred.
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Clackson TP, Chiswell DJ;
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, 1.47e+03;
- Thes 0;
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PT detection of infectious prion proteins or for treating disease such PT as BSE, CJD or scraple
PS Example 9; Fig 6; 99pp; English.

CC W18366-W18285 represent portions of the antibodies of the invention. The CC antibodies of the invention are able to bind the scraple isoform of prion protein prp-Sc in situ. Prions are infectious pathogens that cause CC central nervous system spongiform encephalopathies in humans and animals. CC The scrapie isoform of the prion protein (prp-Sc) is necessary for both the transmission and pathogenesis of the transmissible neurodegenerative CC diseases of animals and humans. The antibodies can be used in a method of the invention for detecting human Prp-Sc in a source. The antibodies specifically bind to prion proteins associated with disease and do not bind to denatured Prp proteins not associated with disease. They can bind to prion proteins of aspecific species of mammals. They can also have the ability to neutralise infectious prions. The antibodies can be used CC for screening for the presence of prions in products such as cc pharmaceuticals, food or cosmetics. They can also be used for prion
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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JAN-1998 (first entry)
prp 28 light chain variable region.
Prion protein; Prp; heavy chain variable region; antibody;
light chain variable region; Prp-Sc; pathogen; fatal famili
central nervous system spongiform encephalopathy; human; th
transmissible neurodegenerative disease; Creutzfeldt-Takob
bovine spongiform encephalopathy; feline spongiform encephalopathy
Serstmann-Strassler-Scheinker Disease.
                                                                                                                                                                                                                                                                         WPI; 97-202357/18.

New antibodies to the scrapie isoform of prion protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 10
W18270
                                                                                                                                                                                                                                                                                                                                              14-SEP-1995; US-528104. (REGC ) UNIV CALIFORNIA. Burton DR, Prusiner SB,
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Local Similarity 100.0%;
hes 5; Conservative
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Pred. No. 1.47e+03
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T asthma, atherosclerosis, AIDS, dementia, etc.

Claim 18; Page 68; 107pp; English.

C This polypeptide comprises the light chain variable region (VL) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VL can be incorporated into a human REI framework to produce a claimed humanised 21.6 VL (see W22412) and a claimed humanised 21.6 vL can be cantibody that is used in the manufacture of a medicament for treating a disease selected from asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumou metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
                                                                                                                                                                                                                                                             29-MAY-1997.
21-NOV-1996; U18807.
21-NOV-1996; US-561521.
4 (ATHE-) ATHENA NEUROSCIENCES INC.
5 Eendig MM, Jones ST, Leger OJ, Saldanha J, Ye
6 WPI; 97-297879/27.
7 N-PSDB; 774759.
8 N-PSDB; 774759.
9 The North of the North of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis;
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Alpha-4 integrin; humanised antibody;
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llarity 100.0%;
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/note- "complementarity determining region
117..126
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d. No. 1.47e+03;
M1smatches 0;
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Inflammatory disease.

Provided to human reshaped antibody 21.6 light CC The sequence represents the human reshaped antibody 21.6 light CC Chain variable region against leukocyte adhesion molecule VLA-4. CC Cloned cDNA sequences of mouse 21.6 VL (99889) and VH (99892) CC regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the CC them subcloned into mammalian cell expression vectors containing then subcloned into mammalian cell expression vectors containing CC human kappa or gamma-1 constant regions. In the humanized light CC chain, amino acids L45, L49, L58 and L69 in the humanized light CC framework are replaced by the amino acid present in the equivalent CC framework are replaced by the amino acid present in the equivalent CC position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into CCS cells. The humanized can be used to inhibit adhesion of a leukocyte to an altibodies can be used to inhibit adhesion of a leukocyte to an stroke, cerebral traumas, meningitis or encephalitis. The contibodies can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The contibodies can also be used for detecting VLA-4, for affinity contification or for generating anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-clair-trauman-anti-cla
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purification or for generating Sequence 126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ATHE-) ATHENA NEUROSCIENCES INC. Bendig MM, Jones TS, Leger OJ, WPI: 95-269276/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUL-1995.
25-JAN-1995; U01219.
25-JAN-1994; US-186269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New humanised antibodies against VLA-4... used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; Q99893
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Similarity 100.0%;
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31 lsas1 35

Mismatches

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Length 126

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Matches
                                                                              The sequence represents the mouse antibody 21.6 light chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned CDNA sequences of mouse 21.6 VL and VH (see Q9992) regions are included to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See Q9985-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids 145, 149, L58 and L69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, creebral traumas, meningitis or encephalitis. The antibodies can also be used for affinity purification or for generating anti-idioture antibodies.
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                                                           anti-idiotype antibodies.
Sequence 126 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-1995; U01219.
25-JAN-1994; US-186269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                                                                 inflammatory disease.
Disclosure; Fig 1; 105pp;
                                                                                                                                                                                                                                                                                                                                                                           New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09519790-A1.
27-JUL-1995.
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Mouse VLA-4 antibody 21.6 light chain variable region.
Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region
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R81326;
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y Match 100.0%;
Local Similarity 100.0%;
hes 5; Conservative
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55..69
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              Score 28; DB 15;
Pred. No. 1.47e+03
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Pred. No. 1.47e+03;
0; Mismatches 0
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r 14 R12237 standard; Protein; 126 AA.

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Matches
                                                                   EP-719859-A1.
03-JUL-1996.
06-DEC-1995; 119233.
20-DEC-1994; EP-120165.
(MERE) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New chimeric mouse human antibodies - used in treatment, diagnosis and prophylaxis of HIV infections.

Disclosure; Fig 13; 108pp; English. ---
The mouse VL gene product may be used to produce chimeric mouse-human Abs against HIV-1 comprising human Ig constant regions and murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections, and may be produced by a bacterial, yeast or mammalian expression system.

Sequence 126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-1991
13-NOV-1990; U06627.
13-NOV-1989; US-433703.
(XOMA-) XOMA COTP.
Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson
WPI: 91-178106/24.
N-PSDB; Q12017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R12237;
19-AUG-1991 (first entry)
WPI; 96-302345/31.
N-PSDB; T35050.
New human integrin V chain-specific monoclonal antibody - and related DNA and hybridomas, for treatment and diagnostic imaging tumours, esp melanoma.
                                                             Adan J, (
Rosell E;
                                                                                                                                                                                                                                                                                  binding_site
                                                                                                                                                                                                                                                                                                                      Mus musculus
Key
                                                                                                                                                                                                                                                                                                                                                          MAb VL17E6 light chain (specific for human alphaV integrins). Monoclonal antibody; MAb; integrin; cell-matrix interaction; tumour; melanoma; glioma; carcinoma; cytokine; interleukin-2;
                                                                                                                                                           region
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R99003;
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                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                          /label= CDR2
77..108
                                                                                                                                                                                                                                     /label= Framework region
70..76
                                                                                                                                                                                                                                                                                                                                                                                                                      Protein; 127
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                                                                                                                                               /label= Framework region
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109..117
                                                                                                                                                                                                                                                                      /label - CDR1
                                                                                                                                                                      'label- CDR3
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Pred. No. 1.47e+03;
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                                                                   Mitjans'F, Piulats
                                                                                                                                                                                              region
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                                                                                                                                                                                                                                                                                                                                                            interleukin-2; IL-2;
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                            Claim 8; Figure 17a; 54pp; English.

A monoclonal antibody which reacts only with the alphav chain of human alphav integrins; which blocks attachment of alphav integrin bearing cells to integrin substrate; which reverses established cell matrix interactions caused by alphav integrin; which blocks tumour development and which has no cytotoxic activity, may be used to treat tumours, especially melanoma (but also glioma, carcinoma) optionally coupled to a cytokine such as interleukin-2. The monoclonal antibody may also be used for diagnostic imaging of tumours and assesment of tumour growth when conjugated to a radiolabel or a radio opaque-agent.

Sequence 127 AA;
  Score 28; DB 20;
Pred. No. 1.47e+03;
0; Mismatches 0
       0
                                                  Length 127
     0
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Search completed: Tue Apr 20 Job time: 18 secs. 13:57:14 1999

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. n on: Tue Apr 20 13:56:19 1999; MasPar time 3.21 Seconds 58.270 Million cell updates/sec

Title:

Description: Perfect Score: >US-08-836-455-2 (31-35) from US08836455.pep (1 of 3) 28

Sequence: 1 LSASL 5

Scoring table: PAM 150 Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

pir58 1:pirl 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 17.008; Variance 14.078; scale 1.208

SUMMARIES

esult	Score	Query Match L	Length	B B	ID	ı۶	. z
1	28	100.0	45	N	S28565	hypothetical protein	6.56e+02
N	28	٠	93	N	S38564	ain V	6.56e+02
ω	28	٠	102	N	S50530	pothetical prot	٠
4	28	٠	106	N	C33936	kappa chain	6.56e+02
υ	28		106	N	PL0259	kappa chain V	6.56e+02
σ	28	100.0	106	N	PL0260	kappa chain V	6.56e+02
7	28	100.0	108	4	B47271	nyl phosp	6.56e+02
8	28	100.0	108	N	C26405	kappa cha	•
9	28	100.0	108	N	B26405	kappa chain V	6.56e+02
10	28	100.0	109	μ	KVMS09	chain V	6.56e+02
11	28	100.0	109		KVMS82	Ig kappa chain V regi	
12	28	100.0	124	N	S03521	chain pr	6.56e+02
13	28		130	Н	KVMSM4	kappa chain	6.56e+02
14	28	100.0	138	N	B69465	transcription regulat	6.56e+02
15	28	100.0	165	N	JE0065	0	6.56e+02
16	28	100.0	177	ν	F70508	probable transmembran	6.56e+02
17	28	100.0	182	N	C71214	hypothetical protein	6.56e+02
18	28	100.0	230	N	S33161	Ig kappa chain – shee	6.56e+02
19	28	100.0	245	N	D71554	probable adenylate cy	6.56e+02
20	28	100.0	268	N	A70417	hypothetical protein	6.56e+02
21	28	100.0	280	N	H71320	hypothetical protein	6.56e+02
22	28	100.0	303	N	B47089	Arac	
23	28	100.0	304	Ν	E45277		6.56e+02

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	
28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
2672	1698	1671	1150	1048	709	685	592	591	576	551	504	452	419	417	412	371	354	352	327	317	
N	N	N	N	N	N	N	N	ผ	N	N	N	N	N	N	N	ผ	N	N	ب	N	ŧ
A48126	S51869	S71628	B47114	S57155	E64213	S64985	S54489	D64204	B71420	S66701	S24314	S77040	A70814	S64006	F64849	C70626	A64894	E71164	S26693	S63358	000
translation activator	probable membrane pro	sensory transduction	phosphoprotein phosph	NMD5 protein - yeast	DNA topoisomerase (EC	hypothetical protein	phosphoribosylaminoim	membrane lipoprotein	hypothetical protein	probable membrane pro	bacterial leucyl amin	hypothetical protein	probable integral mem	hypothetical protein	probable permease b10	hypothetical protein	hypothetical protein	hypothetical protein	transcription factor	hypothetical protein	Thousand thousand for
6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	6.56e+02	0.000

ALIGNMENTS

RESULT 2 ENTRY 19 Kappa chain V region (ASWU1) - mouse (fragment) ORGANISM DATE DATE OGLANISM OGLANISM OGLANISM DATE OGLANISM OGLANISM	Db 8 LSASL 12 	Query Match 100.0%; Score 28; DB 2; Length 45; Best Local Similarity 100.0%; Pred. No. 6.56e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps (#cross-references MUID:94035194 #accession \$28565 ##molecule_type mRNA ##residues 1-45 ##label CAR1 ##cross-references EMBL:X68145; NID:g16178; PID:g16179 ##accession \$31423 ##anolecule_type DNA ##residues 1-45 ##label CAR2 ##cross-references EMBL:X68146; NID:g16330; PID:g16331 ##cross-references EMBL:X68146; NID:g16330; PID:g16331 ##cross-references EMBL:X68146; NID:g16330; PID:g16331	:469-479 thb-2 and -4 genes are strongly induced by ght.	24-Sep-1998 SSIONS S28565; S31423 RENCE S28565 SCATABELLI, M.; Sessa, G.; Baima, S.; Morelli, G.; Ruberti,	cress #variety strain Columbia DATE 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change	S28565 #type complete ENTRY hypothetical protein (Athb-2 5' region) - Arabidopsis thaliana thaliana #common_name mouse-ear
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##CCESSION CJJYJU
##TACTUS preliminary
##status preliminary
##molecule_type mRNA
##residues 1-106 ##label MEE
##cross-references GB:J04577; NID:g623187; PID:g623189
##cross-references GB:J04577; NID:g623187; PID:g623189
CLASSIFICATION #superfamily immunoglobulin v region; immunoglobulin
##CTOSS-references immunoglobulin v region; immunoglobulin
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##cross-references EMBL:U18795; N
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##cross-references EMBL:X75105; NID:g414153; PID:g414154
.FICATION #superfamily immunoglobulin V region; immunog
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Nucleotide changes in sequential variants of influenza virus
hemagglütinin genes and molecular structures of
corresponding monoclonal antibodies specific for each
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Ig kappa chain V region (VM113) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change
08-Sep-1997
                                                                                                                                                                                                                                                  Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; (Proc. Natl. Acad. Sci. U.S.A. (1989) 86:4564-4668
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#length 102
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28-May-1993 #sequence_revision 24-Feb-1995 #text_change
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D.; Marshak-Rothstein, A.; Weigert, M.
J. Exp. Med. (1990) 171:265-297
Anti-DNA antibodies from autoimmune mice
expansion and somatic mutation.
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                                                                                                  #superfamily immunoglobulin V : heterotetramer; immunoglobulin
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If kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
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Anti-DNA antibodies from autoimmune
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#formal_name Mus musculus #common_name house mouse
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##molecule_type protein
1-108 ##label SMI
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#journal Biochemistry (1987) 26:604-612
Complete amino acid sequences of the heavy and light chain variable regions from two A/J mouse antigen nonbinding monoclonal antibodies bearing the predominant p-azophenyl arsonate idiotype.
#cross-references MUID:87157877
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nitrophenyl phosphonate-specific antibody 4867 light chain VJ
- synthetic (fragment)
#formal_name synthetic
Mus musculus (house mouse) gene engineered and expressed in
Escherichia coli
21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change
11-Aug-1995
                                                                                                                            #superfamily immunoglobulin V region;
heterotetramer; immunoglobulin
#length 108 #molecular-weight 11944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C26405 #type complete
Ig kappa chain V region (3D10) - mouse
#formal_name Mus muscullus #common_name house mouse
30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
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Score 28; DB 2; DP 2; DP
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Pred. No. 6.56e+02;
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Pred. No. 6.56e+02
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Blochemistry (1987) 26:604-612
#title Complete amino acid sequences of the heavy and light chal
variable regions from two A/J mouse antigen nonbinding
monocional antibodies bearing the predominant p-azopher
arsonate idiotype.
#cross-references MUID:87157677
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##experimental_source strain A/
(FICATION #superfamily immunoglobulin V region;

TOS heterotetramer; immunoglobulin

#length 108 #molecular-weight 11985
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                                                    h 100.0%;
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Ig kappa chain V region (E109) - mouse
#formal_name Mus musculus #common_name house mouse
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_ch
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The structural basis of a hapten-inhibitable kappa-chain
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J. Immunol. (1979) 122:1905-1910
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Ig kappa chain V region (1F6) - mouse
#formal_name Mus musculus #common_name house
30-Jun-1988 #sequence_revision 30-Jun-1988 #t
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Pred. No. 6.56e+02;
0; Mismatches C
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##residues 1-108 #;
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##residues 1-124 ##label ADZ
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This chain was isolated from a myeloma protein that binds inulin.
An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger
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                                        #length 124 #checksum 9886
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Structure of the variable gene coding for chi-chains of antibodies produced by hybridoma PTF-02.
                                                                                                                                                                                     #superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin
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29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
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*superfamily immunoglobulin V region; immunoglobulin homologyheterotetramer; immunoglobulin
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The complete V domain amino acid sequences of two myeloma inulin-binding proteins.
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Ig kappa chain V region (W3082) - mouse
#formal_name Mus musculus #common_name house mouse
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
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Pred. No. 6.56e+02;
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                                                                                                                              3-22
                                                                                        23-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Gray, W.R.; Dreyer, W.J.; Hood, L.
#journal Science (1967) 155:465-467
#title Mechanism of antibody synthesis: size
#cross-references MUID:67056897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors
#journal
#title
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Matches 5; Conservative
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#title Amino acid sequence of the NH-2-terminal extra piece segments of the precursors of mouse immunoglobulin lambda-1-type and #cross-references MUDI:77148916
#accession A93815
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                                                                                                                                                                                                                                                                                                                                                                                                          ##experimental_source Bence Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type protein
##residues 23-49,')
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##molecule_type DNA
1-117 ##label VK41
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                                                                                                                                                                                                                                                                                                                                                                     19/1
          #length 130
                                                                                                                                                                                                  #superfamily immunoglobulin V region; immunoglobulin homology alternative initiators; heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seidman, J.G.; Max, E.E.; Leder, P.
Nature (1979) 280:370-375

A kappa immunoglobulin gene is formed by site-specific recombination without further somatic mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A94239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A93815
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Ig kappa chain precursor V region (MOPC 41) - mouse
Ig kappa chain precursor V region VK41
#formal_name Mus musculus #common_name house mouse
24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change
                                                                                                                                                                                                                                             oligomers.
                                                                                                                                                                                                                                                          such as IgA and IgM, the subunits associate into larger
                                                                                                                                                                                                                                                                            n immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l6-Aug-1996
#domain immunoglobulin homology #label IMM\
#disulfide_bonds #status predicted
th 130 #molecular-weight 14311 #checksum (
                                                                                                                   #domain signal sequence #status experimental #label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Met-3 is apparently used as 25% of the chains
                                                                #product Ig kappa chain V region (MOPC 41) #status
experimental #label M41\
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                                                                                                         SIG2\
                                                                                                                                                                                                                                                                                                                                                                                                                         1-49, 'B',51-53, 'LSB',57-58, 'ZZ',61-62, 'BZ',65-76, 'B', 78-108,110-130 ##label GRA
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#authors

Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson,
K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.;
Peterson, J.D.; Richardson, D.L.; Kerlavage, A.R.; Graham,
D.E.; Kyrpides, N.C.; Fleischmann, R.D.; Quackenbush, J.;
Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.;
Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman,
J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs,
T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.;
D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.;
Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese,
C.R.; Venter, J.C.
Nature (1997) 390:364-370

#title
Sulfate-reducing archaeon Archaeoglobus fulgidus.
#cross-references MUID:9804943
#accession B69465
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Matches 5; Conservative
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Best Local Similarity 100.0%;
                                                                                                             Johansen, T.; Holm, T.; Bjorklid, E.

#journal Gene (1989) 79:259-267

#title Members of the RTVL-H family of human endogenous

*retrovirus-like elements are expressed in placenta.

*cross-references MIID:90006755

*accession JE0065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-138 ##label KLE ##cross-references GB:AE000984; GB:AE000782; NID:g2689307; PID:g2648831; ##cross-references GB:AF1723
##EXPERIMENTAL_SOURCE placenta :
##experimental_source placenta :
readthrough of the terminator TGA may occur between the
codons GAT for 19-Asp and CGC for 20-Arg
                                                          ##molecule_type mRNA 1888
##molecule_type mRNA 1888
##rostidues 1-165 ##label JOH 1888
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                                                                                                                                                                                                                                                                                                               JEU065 #type fragment
retroviral proteinase-like protein - human (fragment)
#formal_name Homo sapiens #common_name man
31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
24-Feb-1995
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05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
02-Jul-1998
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translation not shown
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		Len 02; 0;	
		Score 28; DB 2; Length 165; Pred. No. 6.56e+02; O; Mismatches O; Indels	
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		0; Gaps	

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Search completed: Tue Apr 20 13:56:36 1999 Job time : 17 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. n on: Tue Apr 20 13:54:52 1999; MasPar time 2.29 Seconds 58.693 Million cell updates/sec

Title: Description: Perfect Score: Sequence: >US-08-836-455-2 (31-35) from US08836455.pep (1 of 3) 28 LSASL 5

Scoring table: PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries Searched: 74019 seqs, 26840295 residues

Database: swiss-prot35 1:swissprot

Statistics: Mean 17.476; Variance 12.170; scale 1.436

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	28	100.0	102	⊢ ¦	YEG9_YEAST	HYPOTHETICAL 11.3 KD P	3.19e+02
2	28	100.0	108	Ь		[N V-V	•
ω	28	100.0	108	_	KV5T_MOUSE	IG KAPPA CHAIN V-V REG	3.19e+02
4	28	100.0	108	_	KV5R_MOUSE	IG KAPPA CHAIN V-V REG	
ر.	28	100.0	125	۳	MFAP_SACKL	MATING FACTOR ALPHA PR	3.19e+02
σ	28	100.0	180	ы	YFXK_BRAJA	HYPOTHETICAL PROTEIN I	3.19e+02
7	28	100.0	255	۳	YFCA_HAEIN	HYPOTHETICAL PROTEIN H	3.19e+02
œ	28	100.0	303	-	ARAL_STRAT	PUTATIVE ARAC-LIKE TRA	3.19e+02
Q	28	100.0	304	ш	ARAL_STRLI	PUTATIVE ARAC-LIKE TRA	3.19e+02
10	28	100.0	317	Ц	YN8F_YEAST	HYPOTHETICAL 35.4 KD P	3.19e+02
11	28	100.0	365	ب	MEFB_HUMAN	MYOCYTE-SPECIFIC ENHAN	
12	28	100.0	367	۲	YMCP_BPF41	HYPOTHETICAL PROTEIN I	3.19e+02
13	28	100.0	371	_	LEU3_SCHPO	3-ISOPROPYLMALATE DEHY	3.19e+02
14	28	100.0	416	Н	MYC_AVIOR	MYC TRANSFORMING PROTE	•
15	28	100.0	416	щ	MYC_CHICK	MYC PROTO-ONCOGENE PRO	•
16	28	100.0	417	ميو	YTFR_ECOLI	HYPOTHETICAL ABC TRANS	3.19e+02
17	28	100.0	417	μ.	YGA4_YEAST	HYPOTHETICAL 46.4 KD T	3.19e+02
18	28	100.0	421	۳	MYC_AVIM2	MYC TRANSFORMING PROTE	3.19e+02
19	28	100.0	422	μ	MYC_AVIMC	MYC TRANSFORMING PROTE	3.19e+02
20	28	100.0	422	4سا	MYC_AVIMD	MYC TRANSFORMING PROTE	3.19e+02
21	28	100.0	443	ب	PORD_PSEAE	PORIN D PRECURSOR (OUT	3.19e+02
22	28	100.0	458	ب	NU4M_PETMA	NADH-UBIQUINONE OXIDOR	3.19e+02
23	28	100.0	479	ب	6PGD_TRYBB	6-PHOSPHOGLUCONATE DEH	3.19e+02

45	44	43	42	41	40	39	38	37	36	35	34	ω 3	32	31	30	29	28	27	26	25	24
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A2MG_RAT	YK76_YEAST	2ACA_HUMAN	NMD5_YEAST	ATHA_HUMAN	PUR2_MOUSE	PWP2_CAEEL	AREA_ASPNG	AREA_EMENI	YSO5_CAEEL	NRFA_PENUR	AREA_PENRO	AMPN_LACDL	MOF_DROME	AREA_PENCH	TOP1_MYCGE	NOLO_RHISN	VE1_PCPV1	CAG2_MOUSE	2ACB_HUMAN	YX23_CAEEL	TCPC_VIBCH
ALPHA-2-MACROGLOBULIN	HYPOTHETICAL 137.5 KD	PROTEIN PHOSPHATASE PP	NONSENSE-MEDIATED MRNA	POTASSIUM-TRANSPORTING	PHOSPHORIBOSYLAMINE G	PERIODIC TRYPTOPHAN PR	NITROGEN REGULATORY PR	NITROGEN REGULATORY PR	HYPOTHETICAL 98.0 KD P	NITROGEN REGULATORY PR	NITROGEN REGULATORY PR	AMINOPEPTIDASE N (EC 3	MALES-ABSENT ON THE FI	NITROGEN REGULATORY PR	DNA TOPOISOMERASE I (E	NODULATION PROTEIN NOL	REPLICATION PROTEIN E1	BETA-1,4 N-ACETYLGALAC	PROTEIN PHOSPHATASE PP	HYPOTHETICAL 59.7 KD P	TOXIN CORREGULATED PIL
3.19e+02	3.19e+02	3.19e+02	3.19e+02	3.19e+02	3.19e+02	3.19e+02			3.19e+02												

ALIGNMENTS

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[1]	٠.).	AIN V-V REG	(REL. 27,	REL 05	13-AUG-1987 (REL. 05, CREATED)		V50	OLT 2		31 I.SAST, 35	70 LSASL 74	Query Match 100.0%; Score 28; DB 1; Length 102; Best Local Similarity 100.0%; Pred. No. 3.19e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1341 MW;	TRANSMEM 70 90 POTENTIAL.		HYPOTHETICAL PROTEIN; TRANSMEMBRANE.	EMBL; U18795; G603259;	SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.	Ξ.		D., NAKAHARA	₽.	ITH S.,	T. CARPENTER J. CHEN E. CHERRY	• •	STRAIN=S288C / AB972:	SEQUENCE FROM N.A.		EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.	SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).		HYPOTHETICAL 11.3 KD PROTEIN IN SOM1-PCM1 INTERGENIC REGION.	(REL. 35, LAST	(REL. 31,	01-FEB-1995 (REL. 31, CREATED)	2:	YEG9 YEAST STANDARD; PRT: 102 AA.

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RESULT 4
ID KV5R_MOUSE
AC P01651;
DT 21-JUL-1986
DT 21-JUL-1986
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                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
ID RESULT
AC POPULATE PROPERTY 21
DT 21
DT 21
DT 21
DT 01
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CO EU
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Best Local s
Matches
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Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                           DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-UUL-1986 (REL. 01, CREATED)
21-UUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
1G KAPPA (CHAIN V-V REGION (W3082).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
PIR; B92811; KVMS82.
HSSP; P01607; IFVD.
                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KV5T_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE: 82099361.
JOHNSON N., SLANKARD J., PAUL L.,
J. IMMUNOL. 128:302-307(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
                                                                                                                                                                     11 LSASL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID NON_TER
                                                                                                                                      31 LSASL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NATURE 304:320-324(1993). MARKHAM A.F.,
-1- ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; K00745; G196455; ... HSSP; P01607; 1FAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 83271467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LSASL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 LSASL 35
                                                                                                                                                                                                        100.0%;
Similarity 100.0%;
5; Conservation
                                                                                                                                                                                                                                                                               108
108
                                                         STANDARD;
                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                    7 REGION.
23
34
49
56
88
97
108
88
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01, CREATED)
01, LAST SEQUENCE
                                                                                                                                                                                                                                                                                   11850
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34
49
56
88
107
107
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                                                                                                                                                                                                      Score
Pred.
0; M
                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
0; 1
                                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING FRAMEWORK 3. COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                             6CA5F4A0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK 4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAMEWORK 1.
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                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
UPDATE)
                                                     108
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3.19e+02;
0;
                                                                                                                                                                                                                                        DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19e+02;
0;
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                                                                                                                                                                                                                                   Length 108;
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                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                               Query Match
Best Local s
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01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUE
01-JAN-1988 (REL. 06, LAST ANNOT
MATING FACTOR ALPHA PRECURSOR (A
SACCHARONYCES KLUYVERI (YEAST).
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                 PEPTIDE
PEPTIDE
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                            SEQUENCE STRAIN-IFO 185., STRAIN-IFO 185., STRAIN-IFO 185., HA)
                                                                                                                               NUCLEIC ACIDS RES. 15:6303-6303(1987).
EMBL; Y00385; G4859; -.
PIR; A29120; A29120
                                                                                                           SIGNAL
                                                                                                                        PHEROMONE; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1993 (REL. 27, 16 KAPPA CHAIN V-V REG. MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHEUTHERIA; RODENTIA, [1]
                                                                                                                                                                                                                                                                 MFAP
                                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEQUENCE
                                                                                                                                                                                                    EUKARYOTA; FUNGI;
                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DISULFID
31
                           Local Similarity 100.0%;
nes 5; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
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DOMAIN
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VRANA M., RUDIKOFF S., POTTER M.

J. IMMUNOL. 122:1905-1910(1979)

-!- THIS CHAIN WAS ISOLATED FRO
                                                                                                                                                                                                                                                                                                 31 LSASL
                                                                                                                                                                                                                                                                                                         11 LSASL 15
LSASL
                                                                                                                                                                                                                                                                                                                                         Local
               LSASL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BETA(2-1)-FRUCTOFURANOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              B92808; KVMS09.
                                                                                                                                                                                                                                                                                                                               100.0%;
Similarity 100.0%;
5; Conservation
               11
                                                                 125 AA;
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                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                 A
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                   V REGION
                                                                                                                                                                                                                      06, CREATED)
06, LAST SEQUENCE UPDATE)
06, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                ASCOMYCOTINA; HEMIASCOMYCETES
                                                               13925
                                                                                                                                                                                                                                                                                                                                                                        23
449
56
88
97
108
108
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REGION (EPC 109)
                                                                                                                                                                                                                                                                                                                                                               11876 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHORDATA; VERTEBRATA;
                                                                                                                        SIGNAL.
                                                               MW;
                          Score 28; DB 1; 1
Pred. No. 3.19e+02;
0; Mismatches (
                                                             POTENTIAL.
                                                                           ALPHA-MATING PHEROMONE.
MATING FACTOR ALPHA (1S
MATING FACTOR ALPHA (2N
POTENTIAL.
                                                                                                                                                                                                                                                                                                                           Score 28; DB 1; I
Pred. No. 3.19e+02;
0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM MYELOMA PROTEINS YL MOIETIES (INULIN).
                                                                                                                                                                                                                                                                                                                                                                                                       FRAMEWORK 1.

COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.

COMPLEMENTARITY-DETERMINING
FRAMEWORK 3.
                                                                                                                                                                                                                  (ALPHA MATING
                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :
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                                                                                                                                                                                                                                                           125
                                                            CRC32;
                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                PHEROMONE).
                           0,
                                           Length 125
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                                                                                                                                                                                                                                                                                                                                           Length 108;
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(2ND
                         Indels
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RESULT 6
ID YFXK_BRAJA
AC P29285;

PRT;

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01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
101-DEC-1992 (REL. 24, LAST ANNOTATION (FRAGMENT).

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Best Local S
Matches
                                                                                                                                                                                                                                                                                               SUBMITTED (SEP-1996) TO EMI-
-!- SUBCELLULAR LOCATION: 1
-!- SIMILARITY: STRONG, TO
-!- SIMILARITY: TO M.LEPRAE
EMBL: U32705; G1573158; -.
TIGR: H10198; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFCA_HAEIN
P46490;
01-NOV-1995
01-NOV-1997
01-NOV-1997
TRANSMEM
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GCCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O., VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, STRAIN-110SPC4;
STRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WHITE O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-RD / KW20; MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTHAMATTEN D., SCHERB B., HENNECK
J. BACTERIOL. 174:2111-2120(1992).
EMBL. M86805; G152086; -.
PIR: A42371; A42371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAEMOPHILUS INFLUENZAE. PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BRADYRHIZOBIUM JAPONICUM. PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                         HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-RD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PASTEURELLACEAE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHIZOBIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 LSASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 LSASL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08;
Similarity 100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REL. 32, CREATED)
(REL. 35, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDAT
L PROTEIN HI0198.
                                    28
76
99
132
153
191
235
                                                                                                                                                                                                                                                                                         PROTEIN;
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                                           48
96
119
152
173
211
                          7 TRANSMEMBRANE.
27 POTENTIAL.
48 POTENTIAL.
96 POTENTIAL.
19 POTENTIAL.
52 POTENTIAL.
53 POTENTIAL.
51 POTENTIAL.
111 POTENTIAL.
111 POTENTIAL.
111 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                            A., KERLAVAGE A.R., FLEISCHMANN R.D., TO EMBL/GENBANK/DDBJ DARA BANKS.
TION: INTEGRAL MEMBRANE PROTEIN (POTEING, TO E.COLI YFCA.
LEPRAE Ull77B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCOTOBACTERIA; AEROBIC RODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Œ.
      ₩.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCOTOBACTERIA; FACULTATIVELY ANAEROBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HENNECKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
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   E5E7023A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; DB 1; No. 3.19e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255
      CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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Best Local
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                                                                                                                PIR; $19843; $19843.

PROSITE: PS00041; HTH_ARAC_FAMILY_1; 1.

PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.

TRANSCRIPTION REGULATION; DNA-BINDING; TRANSPOSABLE ELEMENT.

DNA_BIND 218 237 H-T-H MOTIF (BY SIMILARITY).

SEQUENCE 304 AA; 32878 MW; 6A9C2133 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARAL_STRLI STANDARD; PRT; 304 AA. p35319; 01-JUN-1994 (REL. 29, CREATED) 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) PUTATIVE ARAC-LIKE TRANSCRIPTION REGULATOR. STREPTOMYCES LIVIDANS.
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PROSTTE; PS00041: HTH_ARAC_FAMILY_1; 1.

PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.

TRANSCRIPTION REGULATION; DNA-BINDING.

DNA_BIND 218 237 H-T-H MOTIF (BY S DNA_BIND 218 237 H-T-H MOTIF (BY S SEQUENCE 303 AA; 32309 MW; 1BE5603C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR;
                                                                                                                                                                                                                                                                                                                                                                                                   CHEN C.W., YU T.-W., CHUNG H.-M.,
J. BACTERIOL. 174:7762-7769(1992)
-1- SIMILARITY: BELONGS TO THE AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=66 / 1326;
MEDLINE; 93077460.
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STRAIN-IMRU 3720;
MEDLINE; 93194813.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T.-W., CHEN C.W.;
BACTERIOL. 175:1847-1852(1993)
- SIMILARITY: BELONGS TO THE AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B47089; E
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E19843; S
                                                                                                                                                                                                                                                                                                                                                                             REGULATORS
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Similarity 100.0%;
5; Conservative
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larity 100.0%;
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E45277.
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                                                                                                                                                                                                                                                                                                                                                                                                       ARAC/XYLS FAMILY OF
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                                No.
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No. 3.19e+02;
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3.19e+02
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3.19e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. -F.;
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Best Local S
Matches
                                            SEQUENCE FROM N.A.

ILAMERDIN J.E.;

SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- FUNCTION: TRANSCRIPTION FACTOR WHICH BINDS SPECIFICALLY TO THE MEP2 ELEMENT PRESENT IN THE REGULATORY REGIONS OF MANY MUSCLE-SPECIFIC GENES. ACTIVATES TRANSCRIPTION VIA THIS ELEMENT. MAY BE INVOLVED IN MUSCLE-SPECIFIC AND/OR GROWTH FACTOR-RELATED
           - - -
                                                                                                                                                          POLLOCK R., TREISMAN R.;
GENES DEV. 5:2327-2341(1991).
                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (REL. 32, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RE
PROTEIN 2) (XMEF2) (RSRFR2).
                                                                                                                                                                                                                             NADAL-GINARD B.;
GENES DEV. 6:1783-1798(1992).
                                                                                                                                                                                                                                                               TISSUE-HEART, AND MEDLINE; 92387551
                                                                                                                                                                                     TISSUE-PLACENTA;
MEDLINE; 92084105.
                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; C
                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  MEF2B OR XMEF2
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEFB_HUMAN
Q02080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DA-
-!- CATALYTIC ACTIVITY: ATP + PYRIDOXAL = AL
-!- SIMILARITY: TO OTHER PYRIDOXINE KINASES.
EMBL; Z71642; E239585; -
HYPOTHETICAL PROTEIN; TRANSFERASE; KINASE.
SEQUENCE 317 AA; 35367 MW; 3A4ADB04 CRC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P53727;

01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 35.4 KD PROTEIN IN SEC12-SSK2 IN:
YNR027W OR N3250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 LSASL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31
 TRANSCRIPTION.
SUBGULT: HETERODIMER.
SUBGELLULAR LOCATION: NUCLEAR.
TISSUE SPECIFICITY: EXPRESSED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSASL 35
                                                                                                                                                                                                                                                              BREITBART
                                                                                                                                                                                                                                                                                                                             PRIMATES
                                                                                                                                                                                                            N.A.
                                                                                                                                                                                                                                                                                   AND SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                             R.E.,
                                                                                                                                                                                                                                                                                                                                     CHORDATA;
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ATP + PYRIDOXAL - ADP + PYRIDOXAL
                                                                                                                                                                                                                                                              TOOMS
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Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                     VERTEBRATA;
                                                                                                                                                                                                                                                          L.B.,
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SKELETAL AND CARDIAC MUSCLE
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                                                                                                                                                                                                                                                                                                                                 TETRAPODA; MAMMALIA;
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                                                                                                                                                                                                                                                         MAHDAVI V.,
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Best Local S
Matches
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE; 91285421.
CHUNG D.K., KIM J.H., BATT C.A.;
GENE 101:121-125(1991).
EMBL; M37979; : NOT_ANNOTATED_CDS.
PIR; PE0401: PE0401.
HYPOTHETICAL PROTEIN.
NON_TER 367 367
SEQUENCE 367 AA; 39163 MW; FBD3Df
                                                                                                                                                                                                                                                                            LEU3_SCHPO STAN
P18869;
01-NOV-1990 (REL. 1
01-NOV-1990 (REL. 1
01-NOV-1995 (REL. 3
3-ISOPROPYLMALATE D
SEQUENCE FROM N.A.

MEDILINE; 89106270.

KIKUCHI Y., KITAZAWA Y., SHIMATAKE G., YAMAMOTO M.;

KIKUCHI Y., KITAZAWA Y., SHIMATAKE G., YAMAMOTO M.;

CURR. GENET. 14.375-379(1988).

-!- CATALYTIC ACTIVITY: 3-CARBOXY-2-HYDROXY-4-METHYLPENTANOATE

NAD(+) = 3-CARBOXY-4-METHYL-2-OXOPENTANOATE + NADH (THE PRO
DECARBOXYLATES TO 4-METHYL-2-OXOPENTANOATE).
                                                                                                                                                                                                               SCHIZOSACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YMCP_BPF41
P26812;
01-AUG-1992
01-AUG-1992
01-AUG-1992
                                                                                                                                                                                               EUKARYOTA;
                                                                                                                                                                                                                                              LEU1
                                                                                                                                                                                                                                                          (IMDH) (3-IPM-DH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN IN MCP 3' REGION (FRAGMENT).
LACTOCOCCUS LACTIS BACTERIOPHAGE F4-1.
VIRIDAE; NOT YET CLASSIFIED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 LSASL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACTORS (MADS-DOMAIN).
EMBL; X68502; G37992; -
EMBL; X63380; G36169; -
EMBL; AC002126; G2329909;
MIM; 600661; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
TRANSCRIPTION REGULATION; NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 LSASL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE MEF2 SUBFAMILY OF MADS PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 LSASL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 LSASL 35
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Local Similarity 100.0%;
les 5; Community 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n 100.0%;
Similarity 100.0%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                       16, CREATED)
16, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE)
DEHYDROGENASE (EC 1.1.1.85)
                                                                                                                                                                                 2S POMBE (FISSION YEAST).
ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
86
31
38638
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Pred. No.
0; Misma
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Pred.
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MEF2-TYPE
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                                                                                                                                                                                                                                                                                                                                                                                       371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.19e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367
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( (BASIC).
(B1 CRC32;
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RESULTANCE OF COLORS OF CO
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Best Local s
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                               MYC PROTO-ONCOGENE PROTEIN (

MYC_CHICK STANDARD;

P01109;

21-JUL-1986 (REL. 01, CARST S

21-JUL-1996 (REL. 01, LAST S

01-OCT-1996 (REL. 34, LAST A

MYC PROTO-ONCOGENE PROTEIN (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: THIRD STEP IN LEUCINE BIOSYNTHESIS.
-!- SUBGUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBGULLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE DEHYDROGENASES FAMILY.
EMBL; M36910; G173412; -.
HSSP; P00351; 1HEX.
PROSITE; PS00470; IDH_IMDH; 1.
OXIDOREDUCTASE; LEUCINE BIOSYNTHESIS; NAD.
SEQUENCE 371 AA; 39732 MW; DAEF72EA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00038; HELIX, LOOP HELIX; 1.
TRANSFORMING PROTEIN; NUCLEAR PROTEIN; DNA-BINDING;
DNA_BIND 331 384 HELIX-LOOP-HELIX MOTIF
SEQUENCE 416 AA; 46040 MW; 7040632F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLICK: 85190568.

HAYFILICK J., SEEBURG P.H., OHLSSON R., PFEIFER-OHLSSON S.,

WATSON D., PAPAS T., DUESBERG P.H.;

PROC. NATL. ACAD. SCI. U.S.A. 82:2718-2722(1985).

-!- THIS PROTEIN IS SYNTHESIZED AS A GAG-MYC POLYPROTEIN.

-!- SIMILARITY: TO OTHER MEMBERS OF THE MYC FAMILY OF HELIX-LOOP-HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYC_AVIOK STANDARD; PRT; 416 AA. P12523; O1-OCT-1989 (REL. 12, CREATED) O1-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE) O1-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE) MYC TRANSFORMING PROTEIN.
                               SEQUENCE FROM N.A.
MEDLINE; 83169838.
WATSON D.K., REDDY E.P.,
PROC. NATL. ACAD. SCI. U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M11352; G209657; -. PIR; A22669; TVFVAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIRIDAE; SS-RNA ENVELOPED ONCOVIRINAE.
                                                                                                                                                                                                                                                                       GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVIAN RETROVIRUS
                                                                                                                                                                                                                                   GALLIFORMES
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Similarity 100.0%;
5; Conservative
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Similarity 100.0%;
5; Conservative
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                                                                                                                                                                                                                                                                       CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENT ANNO
                                       DUESBERG P.H., PAPAS T.S.S.A. 80:2146-2150(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                   (C-MYC).
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE UPDATE)
ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28; DB 1; I
Pred. No. 3.19e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28; I
Pred. No. 3.
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                                                                                                                                                                                                                                                                       VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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3.19e+02;
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                                                                                                                         Matches
                                                                                                                                                    Query Match
Best Local :
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DNA_BIND
CARBOHYD
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TRANSFAC; T00141; ...
PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
PROTO-ONCOGENE; NUCLEAR PROTEIN; DNA-BINDING; PHOSPHORYLATION;
PROTO-ONCOGENE; NUCLEAR PROTEIN, DNA-BINDING; PHOSPHORYLATION;
PROTO-ONCOGENE; NUCLEAR PROTEIN, ACTIVATOR; GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHIH C.-K., LINIAL M., GOODENOW M.M., HAYWARD W.S.;
PROC. NATL. ACAD. SCI. U.S.A. 81:4697-4701(1984).
-I- FUNCTION: PARTICIPATES IN THE REGULATION OF GENE TRANSCRIPTION.
-EINDS DNA BOTH IN A NON-SPECIFIC MANNER AND ALSO SPECIFICALLY T
RECOGNIZES THE CORE SEQUENCE CAC[GA]TG. SEEMS TO ACTIVATE THE
TRANSCRIPTION OF GROWTH-RELATED GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: TO OTHER MEMBERS TRANSCRIPTION FACTORS.
EMBL; J00889; G212355; -.
EMBL; M20006; G211566; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 88302180.
HAHN M., HAYWARD W.;
MOL. CELL. BIOL. 8:2659-2662(1988).
                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: BINDS DNA AS AN HETERODIMER WITH MAX.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- DISEASE: OVEREXPRESSION OF C-MYC IS IMPLICATED A VARIETY OF HEMATOPOIETIC TUMORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-44 FROM N.A. MEDLINE; 84272700.
                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                         Local Similarity 100.08 hes 5; Conservative
   31 LSASL
                                                            3 LSASL 7
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      35
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163
183
398
331
61
416 AA;
                                                                                                                                                 100.0%;
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167
186
401
384
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                                                                                                                                                                                                                                          MW;
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Pred.
0; M
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POLY-PRO.
POLY-ALA.
POLY-ARG.
                                                                                                                                                                                                                                HELIX-LOOP-HELIX MOTIF (BY GLCNAC (BY SIMILARITY).; D761BBCB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF THE MYC FAMILY
                                                                                                                         Mismatches
                                                                                                                                                    28; DB 1; I
No. 3.19e+02;
                                                                                                                                                                             Length 416;
                                                                                                                         0
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. n on: Tue Apr 20 13:55:19 1999; MasPar time 4.54 Seconds 54.879 Million cell updates/sec

Sequence: Description: Perfect Score: Title: >US-08-836-455-2 (31-35) from US08836455.pep (1 of 3) 1 LSASL 5

Searched: Scoring table: PAM 150 Gap 11 165420 segs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb16

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 16.819; Variance 13.365; scale 1.258

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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357	354	352	350	340	328	307	286	268	241	221	212	204	182	166	154	138	132	45	Length
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HYPOTHETICAL 39.8 KD P	FROM BASES 1485094 TO	352AA LONG HYPOTHETICA	CHLOROPHYLL A/B ANTENN	YVBQ PROTEIN.	CATIONIC AMINO ACID TR	ORF YDL119C.	DIPEPTIDE ABC TRANSPOR	HYPOTHETICAL 30.4 KD P	ANTI-CEA 79 SINGLE CHA	HYPOTHETICAL 23.4 KD P	CONSERVED HYPOTHETICAL	LEUKEMIA INHIBITORY FA	182AA LONG HYPOTHETICA	NEUTRAL PROTEASE LARGE	HYPOTHETICAL 17.5 KD P	TRANSCRIPTIONAL REGULA	HYPOTHETICAL 14.0 KD P	HYPOTHETICAL 5.1 KD P	Description
7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	7.03e+02	Pred. No.

.0 371 2 P96353 DAPE .0 417 2 P72417 HSDM .0 419 2 O53861 PUTA* .0 421 4 Q00089 MYC 0 .0 452 2 Q55962 HYPO .0 452 11 O54858 CARB .0 652 11 O54859 CARB .0 652 11 O54859 CARB .0 652 11 O54859 CARB .0 654 11 O54859 CARB .0 657 14 O56221 PROTI .0 934 4 O6622 PROTI .0 934 4 O6622 PROTI .0 1104 14 P90356 DAR .0 1107 14 Q88919 RNA .0 1106 10 O22476 MICRB .0 1295 2 O68900 REPL .0 1596 14 Q66220 REPL .0 1596 14 Q66220 REPL .0 1596 14 Q66220 REPL .0 1648 14 P89877 186K	G,	4	ω	N	~	0	9	œ	7	σ	UI	4	w	N	_	0	29 2	œ	7	o	ر.	4	w	N	_
2 P96353 HYPOTHETICAL 4 2 O32633 DAPE. 2 O32633 DAPE. 2 P72417 HSDM, HSDS 6 H 2 P72417 HSDM, HSDS 6 H 2 O53861 PUTATIVE MEMBR 14 Q000089 MYC TRANSFORMI 2 Q55962 HYPOTHETICAL 4 3 O59785 HYPOTHETICAL 5 14 O39279 COUNTERPART DA 11 O54858 CARBOXYPEPTIDA 11 O54859 CARBOXYPEPTIDA 11 O54859 CARBOXYPEPTIDA 11 O56262 PROTOCADHERIN 11 P97660 RINI. 14 O56221 PROTOCADHERIN 12 P74693 ACRIFLAVINE RE 14 O66622 PROTOCADHERIN 14 Q68925 DANA POLYMERASE 14 Q88915 RIA REPLICASE 14 P90356 129K PROTEIN. 10 O22476 MICROCYSTIN SY 2 O68900 PET PRECURSOR: 14 Q88920 RAR REPLICASE 14 P89877 186K PROTEIN.	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
DAPE. HYPOTHETICAL 4 DAPE. HSDM, HSDS 6 H HSDM, HSDS 6 H PUTATIVE MEMBR MYC TRANSFORMI HYPOTHETICAL 5 COUNTERPART OF CARBOXYEPETIDA DAA FOLYMERASE RNA REPLICASE BRASSINOSTEROI MICROCYSTIN SY PET PRECURSOR. REPLICASE. RNA REPLICASE																									371 2
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	186K PROTEIN.	REPLICASE	REPLICASE.	PET PRECURSOR.	MICROCYSTIN SYNTHETASE		129K PROTEIN.	REPLICASE	POLYMERASE (EC	ORF42.	PROTOCADHERIN 43.		P110.	RIN1.	FROM CHROMOSOME			OF HSV-1	56.8 KD	48.0 KD		MEMBRANE	, HSDS & HSDR	DAPE.	40.2 KD

ALIGNMENTS

RN [1] RP SEQUENCE FROM N.A. RC STRAIN=IRELAND; RA POLOGMIENKO A., KRELL P.; RL SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.	DT 01-JUL-1997 (TREMBLREL. 04, CREATED) DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE) DT 01-JUL-1997 (TREMBLREL. 07, LAST ANNOTATION UPDATE) DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE) DE HYPOTHETICAL 14.0 KD PROTEIN. OS CHORISTONEURA FULLFERANA NUCLEAR POLYHEDROSIS VIRUS (CFMNPV). OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; BACULOVIRIDAE; EUBACULOVIRINAE	SU	31 LSASL	Db 8 LSASL 12	Query Match 100.0%; Score 28; DB 10; Length 45; Best Local Similarity 100.0%; Pred. No. 7.03e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; O	NW HYPOTHETICAL PROTEIN. SQ SEQUENCE 45 AA; 5101 MW; F66824F4 CRC32;	PLANT J. 4:469-479(1993). EMBL; X68145; G16179; FWD: X68145; G16179;	RP SEQUENCE FROM N.A. RC STRAIN=COLUMBIA;		01-NOV-1996 (TREMBLREL 01, LAST SEQUE 01-FEB-1997 (TREMBLREL 02, LAST ANNOT HYPOTHETICAL 5.1 KD PROTEIN IN ATHB-2 ARABIDOPSIS THALLANA (MOUSE-BAR CRESS)	Q05480; 01-NOV-1996 (TREMBLREL: 01, CREAT	RESULT 1 ID Q05480 PRELIMINARY; PRT; 45 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A KLENKH.-P., CLAYTON R.A., TOMB J.-P.,-WHITE O., NELSON K.E.,

A KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

A KICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,

A FLEISCHMANN R.D., QUACKEBHUSH J., LEE N.H., SUTTON G.G., GILL S.,

A KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,

A PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,

A OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,

A COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,

SADOW P.M., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,

ANASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,

NATURE 390:364-370(1997).

RUML, AED009984; G2648831; -.

TIGR; AE1723; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQ
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Best Local
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ŚEQUENCE FROM N.A.

STRAIN-PCC6803;

KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,

MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,

HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA
                                                                                                                                                                                                                                                                         01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
HYPOTHETICAL 17.5 KD PROTEIN.
SYNECHOCYSTIS SP.
EUBACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tches
                                                                                                                                                                     SUBMITTED
                                                                                                                                                                                            STRAIN-PCC6803;
TABATA S.;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               P74274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-VC-16 / DSM
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ARCHAEBACTERIA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSCRIPTIONAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LSASL (
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Local Similarity 100.0%;
les 5; Conservative
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                                                                                                                                                                ТО
                                                                                                                                                   EMBL/GENBANK/DDBJ DATA BANKS
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, LAST ANNOTATION UPDATE)
PROTEIN, ASNC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28; DB 1; Ler
Pred. No. 7.03e+02;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525B1B91 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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7.03e+02;
0;
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      Query Match
Best Local S
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057725;
057725;
01-AUG-1998 (TREMBLREL 07,
I 01-AUG-1998 (TREMBLEEL 07,
O1 AUG-1998 (TREMBLEEL 07,
O1 AUG-1998 (TREMBLEEL 07,
O1 AUG-1998 (TREMBLEEL 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
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Best Local S
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Best Local s
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GENE 79:259-267(1989).
EMBL; M27826; G804764;
PFAM; PF00077; rvp.
                                                                                                                                                                                                                                      KAWARABAYAŚI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y., YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y., SAKAI M., OGURA K., OTSUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI AOKI K., YOSHIZAWA T., NAKAMURA Y., MASUCHI Y., SHIZUYA H.,
                                                                                                                        SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; AB009464; D1027108; -. SEQUENCE 182 AA; 19120 MW; A4F6EDEC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARCHAEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q15408 PRELIMINARY; PRT; 166 AA.
Q15408;
Q1-NOV-1996 (TREMBLREL. 01, CREATED)
O1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
O1-UN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
NEUTRAL PROTEASE LARGE SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                  KIKUCHI H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-OT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYROCOCCUS HORIKOSHII. ARCHAEA; EURYARCHAEOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA; (
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-PLACENTA;
MEDLINE; 90006755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 LSASL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 LSASL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 LSASL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 LSASL 88
n 100.0%;
Similarity 100.0%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Similarity 100.0%;
5; Conservative
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BJORKLID
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07, LAST
07, LAST
PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THERMOCOCCALES; THERMOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Œ;
Score 28; DB 1; I
Pred. No. 7.03e+02;
0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No.
0; Misma
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Pred. No.
0; Misma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1DE57D18 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
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. 7.03e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; I
7.03e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ⋧
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                                                        Length 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYROCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YASUDA
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Matches
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Best Local :
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                                                                                                                                           VENTER J.C.;
VENTER J.C.;
VENTER J.C.;
VENTER 390:364-370(1997)...
EMBL; ABE001016; G2649299; -.
TIGR; AF1282; -.
HYPOTHETICAL PROTEIN.
**FOURENCE 212 AA; 24708 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Q64015;
                                                                                                                                                                                                                                         KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E., KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C., RICHARDSON D.L., COMMANDES J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F., DOUGHERIY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S., REICH C.I., MCNRILL L.K., BADGER J.H., GLODEK A., ZHOU L., OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T., COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TREMBLREL 05, CRE
01-JAN-1998 (TREMBLREL 07, LAS'
01-JAG-1998 (TREMBLREL 07, LAS'
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSU L.W., HEATH J.K.;
BIOCHEM. J. 302:103-110(1994).
EMBL; S73374; G663150; -.
MGD; WGI:96787; LIF.
PROSITE; PS00590; LIF_OSM; 1.
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 98049343.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-VC-16 / DSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARCHAEBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARCHAEOGLOBUS FULGIDUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    028986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 94347086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLREL. 01, 01-NOV-1996 (TREMBLREL. 01, 01-JUN-1998 (TREMBLREL. 06, LEUKEMIA INHIBITORY FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 LSASL 118
                                                                134 LSASL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 100.0%;
Local Similarity 100.0%;
                                                                                            Match 100.0%;
Local Similarity 100.0%;
les 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIF_OSM; 1.; 22485 MW;
                                                                                                                                                       ₩;
                                                                                                                                                                                                                                                                                                                                                                                                               ATCC 49558;
                                                                                         Score 28, DB 1;
Pred. No. 7.03e+0
0; Mismatches,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAST ANNOTATION UPDATE)
(LIF-LEUKEMIA INHIBITORY FACTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB 11; Le
Pred. No. 7.03e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                       C3267F18 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8E590658 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE UPDATE
212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204
                                                                                                          DB 1; L
7.03e+02;
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                                                                                                                        Length 212;
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                                                                                            Indels
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                                                                                            Gaps
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RESULT 11 ID 067364 AC 067364; DT 01-AUG-1998

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                                                                                                                                           Query Match
Best Local S
Matches
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Best Local Similarity 100.0%;
Matches 5; Conservative
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P97771;

P97771;

P97771;

O1-MAY-1997 (TREMBLREL. 03, C1
O1-MAY-1997 (TREMBLREL. 03, L1
O1-UN-1998 (TREMBLREL. 06, L1
ANTI-CEA 79 SINGLE CHAIN FV FI
MUS MUSCULUS (MOUSE).

EUKARYOTA: METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                    CHUNG J.H., LEE S.D., YI K.S., SUH P.G., RYU S.H., CH
KIMIJ., CHOI I.H., CHUNG H.K.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; U88067; G1850548; -.
PEPAM; PF00047; 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
HARRISON D., HOANG L., KEBGLE P., LUMM W., POTHIER B., QIU D.,
SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
JUWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
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                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHANOBACTERIUM THERMOAUTOTROPHICUM ARCHAEBACTERIA; EURYARCHAEOTA; METHAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            026628;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M., DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.; J. BACTERIOL. 179;7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 98037514.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METHANOBACTERIACEAE.
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                                              144 LSASL 148
   31 LSASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31
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                                                                                                                                   100.0%;
Similarity 100.0%;
5; Conservati
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   35
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                                                                                                                                                                                                                                                                                               241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TREMBLREL. 05, CREATED)
(TREMBLREL. 05, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                               241
26086 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23425 MW;
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                                                                                                                                           Score 28; DB 11;
Pred. No. 7.03e+0
0; Mismatches
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 7.03e+02
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT (FRAGMENT).
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                                                                                                                                                                                                                                                                                                   EBB2D29D CRC32;
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                                                                                                                                               Indels
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                                                                                                                                               Gaps
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RESULT
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AC 02
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RN GS SI
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Best Local S
Matches
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01-AUG-1998 (
HYPOTHETICAL
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01-JAN-1998
01-AUG-1998
                                                                                                                                                                                             MEDLINE; 98049343.

KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E., KETCHUM K.A., DOSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C., FLEISCHHANN R.D., OUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., ELGICHARDSON D.L., OUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU JOYERBEEK R., GOCAYME J.D., WEIDMAN J.F., MCONNALD L., UTTERBACK T., COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
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DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LE
DECKERT G., WARREN P.V., SNEAD M.A., KELLER M., AUJAY
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AE000736; G2283776; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 268 AA; 30387 MW; E6FF0262 CRC32;
                                                                                                                              VENTER J.C.;
NATURE 390:364-370(1997).
EMBL; AE000980; G2648779; -.
TIGR; AF1769; -.
PFAM; PF00528; BPD_transp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-VF5;
DECKERT G., WARREN P.V., GAASTERLAND T
GRAHAM D.E., OVERBEEK R., SNEAD M.A.,
FELDMAN R.A., SHORT J.M., OLSON G.J.,
NATURE 392:353-358(1998).
                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      028505;
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AQUIFEX AEOLICUS.
                                                                                                                       HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      028505
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                                                                                                                                                                                                                                                                                                                                                                                       ARCHAEOGLOBUS FULGIDUS.
ARCHAEBACTERIA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 LSASL 250
                                                                Match 100.0%;
Local Similarity 100.0%;
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Local Similarity 100.0%;
les 5; Conservation
                          91
 31
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            LISASL 95
 LSASL 35
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GIREMBLREL.
GIREMBLREL.
                                                                                                          286 AA;
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(TREMBLREL. 07, I
L 30.4 KD PROTEIN.
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                                                     Conservative
                                                                                                                       PROTEIN.
                                                                                                                                                                                                                                                                                                                                                    DSM 4304 / ATCC 49558;
                                                                                                          30810 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                           05, CREATED)
05, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28;
Pred. No. 7
                                                  Score 28;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                         BB200F80 CRC32;
                                                     Mismatches
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ANNOTATION UPDATE)
                                                                 No. 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; L
7.03e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286
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                                                                              DB 1;
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                                                                   .03e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                              Length 286;
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                                                     0;
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ZHOU L.,
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RESULT IN A CONTROL OF THE CONTROL O
RESULT
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AC 03
DT 01
DT 01
DT 01
DT 11
OF Y1
GN Y1
OS BJ
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Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                       ULT 15
032253 PRELIMINARY;
032253;
01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
01-AUG-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
Q07534
Q07534;
Q07534;
Q1-NOV-1996
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NON_TER
NON_TER
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060458;
060458;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
CATIONIC AMINO ACID TRANSPORTER-1 (FRAGMENT).
CRICETULUS GRISEUS (CHINESE HAMSTER).
CRICETULUS GRISEUS (CHINESE HAMSTER).
CRICETOLIS RETAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WANG H., KLAMO E., KUHMANN S.E., KOZAK S., KAVANAUGH M.P., SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; U49797; G1469943; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANI INNER MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TREMBLREL. (ORF YDL119C. SACCHAROMYCES CEREVISIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00153; mito_carr.
MITOCHONDRION; REPEAT; TRANSMEMBRANE; TF
SEQUENCE 307 AA; 34203 MW; CB15B354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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                                                                   YVBQ PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-OVARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA;
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                                                                                                                                                                                                                                                                                                                                                                                                                         232 LSASL 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JUL-1996)
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328 AA;
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llarity 100.0%;
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35208
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ASCOMYCOTINA; HI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WW;
                                                                                          LAST SEQUENCE UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28; DB 11;
Pred. No. 7.03e+02;
0; Mismatches (
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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No. 7.03e+02
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MEMBRANE PROTEIN.
                                                                                                                                                                                                                             340
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DATA BANKS.
                                                                                                 UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 328;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RA AZEYEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA BORRISS R., BOURSIER L., BRAN, A., BRAUN M., BRIGBELL S.C., BRON S.,
RA BORRISS R., BRUSCHI C.V., CALLWELL B., CAPUANO V., CARTER N.M.,
RA BROUILLET S., BRUSCHI C.V., CALLWELL B., CAPUANO V., CARTER N.M.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CHALLCH S.D., EMMERSON P.T.,
RA CHOILOTT F., DEVINE K.M., DUSTERHOFT A., EHALICH S.D., EMMERSON P.T.,
RA CHOILOTT F., DEVINE K.M., DUSTERHOFT A., GALLERON N., GHIM S.Y.,
RA CHOILOT F., DEVINE K.M., DUSTERHOFT A., GALLERON N., GHIM S.Y.,
RA CHOILOT F., DEVINE K.M., DUSTERHOFT A., HILBERT H.,
RA CHILLAN K.D., ERRINGTON J., FABREY C., FERNARI E., FOULGER D., FRITZ C.,
RA FUJITA M., FUJITA Y., FUMA S., GALLERON N., GHIM S.Y.,
RA GLASER P., GOFFEAU A., GOLLIGHTLY E.J., GRANDI G., GUISEPPI G.,
RA GUY B.J., HAGA K., HAICCH J., HARWOOD C.R., HENAUT A., HILBERT H.,
RA HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L., JORIS B.,
RA KOETTER P., KONINGSTEIN G., KROGH S.N., KUMANO M., KURITA K., LAPIDUS A.,
RA KARMATA D., KASAHARA Y., KLAZAREVIC.V., LEE S.M., LEVINE A., LIU H.,
RA KARMATA D., NAKAI S., NOBACK M., MEDIKAN N., MELLADO R.P., MIZUNO M.,
MOESTI D., NAKAI S., NOBACK M., MEDIKAN N., MELLADO R.P., MIZUNO M.,
MOESTI D., NAKAI S., NOBACK M., PRESECAN E., PUJIC P., PURNELLE B.,
RA RAPOPORT G., REY M., REYNOLDS S., RIEGER M., RIVOLITA C., ROCHA E.,
RA RAPOPORT G., SHIN B.S., SOLDO B., SOROKIN M., RIVOLITA C., ROCHA E.,
RA RAPORTA P., TOKNOH P., SEKIGUCHI J., SEKOWSKA A., SEROR S.J.,
RA SCHROETER R., SCOFFONE F., SEKIGUCHI J., SEKOWSKA A., SEROR S.J.,
RA YANNUER F., VASAFOTTI A., VIANTA A., VANABUTT R., WEDLER E., WEDLER H.,
RA YANNUER F., VASAFOTTI A., VIANTA A., YANAMOTO H., YAMANE K.,
RA YANNUER F., SOLOD B., SOROKIN A., YANAMOTO H., YAMANE K.,
RA YANNUER F., SOLOD B., SOROKIN A., YANAMOTO H.
                                                                                                                                                                                                                                Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                       KUNST F., ÓGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBARK/DDBJ DATA BANKS.
EMBL; Z99121; E1186083; - EMBL; Z99121; E1186083; - 65C3FE2D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NATURE 390:249-256(1997).
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completed: Tue Apr 20\ 13:56:00\ 1999 ne : 41\ secs.
                                                                                                                                                                     40 LSASL 44
                                                                                                                                                                                                                             Match 100.0%;
Local Similarity 100.0%;
les 5; Conservative
                                                                                                                31 LSASL 35
                                                                                                                                                                                                                          Score 28; DB 2; Length 340; Pred. No. 7.03e+02; 0; Mismatches 0; Indels
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71 70 66	73 72 72	70 70 70 70	776666	788 778 766
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26 4	6006	114 75	2623218	2226618
R39265 R64204 R21292	R30776 W00373 R99003 R32121	R09426 R53340 R33257 R84553 R60206	R52039 R12237 W11815 R12359 R12359 R29010 W06215	R52040 R28670 R52865 R80079 R30768 W16620 W00834
se Coclor	H52L6-158 murine anti- Anti-CD18 chimeric an MAb VL17E6 light chai Anti-CD4 antibody MT	ight Chain V H chain vari mmunoglobulin CH94.03 light cific CD3-L6F		hain variable protein produ fluenza N10 s erived light anti-CD3 MAb man FasL anti-Chain light chain
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ALIGNMENTS

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W09722699-A2.
26-JUN-1997.
19-DEC-1996; U20757.
13-DEC-1996; US-575762.
20-DEC-1996; US-575762.
26-JAN-1996; US-591965.
(KENT) UNIV KENTUCKY.
Chatterjee M, Chatterjee SK, I
                                                                                             Region
                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                  W7119 standard; Protein; 145 AA.
W27119;
W27119;
04-JAN-1998 (first entry)
Murine monoclonal anti-idiotype antibody 11D10 VL region.
Monoclonal antibody 11D10; anti-idiotype antibody; mucin;
human milk fat globule; HMFG; tumour; breast cancer; vaccine.
                                                                                                                                                    Region
                                                                                                                                                                                Region
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                                                                                                                                                                                                                                                                                                                 Mus musculus.
Key
                                                                                                                         Region
                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                       Peptide
                                                                       77..108
77..108
77..108
77..108
78.109
79..117
71abel= CDR3
70te= "complementarity determining region 3"
718..127
71abel= FR1
70te= "framework region 4"
                                                                                                                                                                                                                                                                                      /label= Sig_peptide
21..145
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                         /label= FR2
/note= "framework region 2"
                                                                                                                                                                                                              Nabel- CDR1
                                                                                                                                                                                                                                                /label= FR1
/note= "framework region 1"
                                                                                                                                                                                                                                                                           /label = Mat_protein
                                                                                                                                                           'Label= CDR2
'note= "complementarity determining region 2"
   Foon KA;
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RESULT
ID WZ
AC WZ
AC WZ
DT 04
DE MU
KW MC
KW MC
KW MC
FH K¢
FT R¢
FT R¢
FT R¢
PT Monocional anti-idiotype antibody 11D10 - elicits immune response pragainst human milk fat globule disease associated tumours, especially breast cancer PS Example 2; Fig 26C; 130pp; English.

CI This polypeptide sequence comprises a consensus sequence of murine C light chain variable regions (VL) selected on the basis of identity C light chain variable regions (VL) selected on the basis of identity C light chain variable regions (VL) selected on the basis of identity C light chain variable regions (VL) selected on the basis of identity C light chain the variable regions (VL) selected on the basis of identity C light variable regions (W27129) was also produced. Illing has at C search. A VH consensus (W27122) was also produced. Illing has at C least 18 departures from the consensus sequences (7 in the light C chain and I in the heavy chain). 8 Occur within CDRs and 10 cutside CDRs. Illing polypeptides and polynucleotides can be used in vaccines and pharmaceutical compositions for the treatment CC outside CDRs and pharmaceutical compositions for the treatment CC of human milk fat globule-associated diseases such as breast
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Sc Claim 9; Page 94; 130pp; English.

CC This polypeptide sequence comprises the light chain variable region

CC (VL) of monoclonal anti-idiotype antibody 11D10 produced by

Noridoma cell line ATCC 12020. 11D10 was obtained by immunising

CC naive mice with MC-10 anti-immune response against a specific epitope

CC response. It elicits an immune response against a specific epitope

CC of a high mol.wt. mucin of human milk fat globule (HMFG). It

CC and patients with advanced HMFG-associated tumours. Pharmaceutical

CC and patients with advanced HMFG-associated tumours. Pharmaceutical

CC and/or 11D10 polynucleotides (see also 785149-50) are claimed.

CC and/or 11D10 polynucleotides (see also 785149-50) are claimed.

CC treating HMFG-associated tumours. 11D10 is also used in a claimed

CC treating HMFG-associated tumours. 11D10 is also used in a claimed

CC method of palliating HMFG-associated disease and in claimed kits to

CC common to the composition of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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19-DEC-1996; U20757.
13-DEC-1996; US-575762.
20-DEC-1995; US-575762.
26-JAN-1996; US-591965.
                                                                                                                                                                                                                                                                                                                                                                                                                 Chatterjee M, Ch
WPI; 97-341690/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine antibody light chain variable region consensus. Monoclonal antibody 11D10; anti-idiotype antibody; mucin; human milk fat globule; HMFG; tumour; breast cancer; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KENT ) UNIV KENTUCKY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus.
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W27121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
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Similarity 100.0%
17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Chatterjee SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "complementarity determining region
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'note= "complementarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0%;
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Pred.
0; M
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d. No. 3.18e-05;
Mismatches 0;
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Matches 1
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10-JUL-1991; G01134.
10-JUL-1990; GB-015198.
10-GCT-1990; GB-022845.
11-GCT-1990; GB-024503.
06-MAR-1991; GB-004744.
15-MAY-1991; GB-004744.
(CAMB-) CAMBRIDGE ANTIBODY.
(MEDI-) MED RES COUNCIL.
                                                                                                            chain was also amplified from an existing construct, PSWI-VHDI.3 (Ward et al, 1989). The two fragments were assembled via a linker vector for expression on the surface of fd bacteriophage. In this way, the VL domain was replaced by a library of VL domains to allow clones were isolated which bound to TEL (the parent antibody Dl.3 two of these clones, WFI to HEL). The sequences of the light chains of respectively. The Dl.3 light chain is given in R21310 and R21311 see also R21260-307, 309-312, R22450, R22565, R22567-81.
                                                                                                                                                                                                                                                                                                                                                                                                                          Producing members of specific binding pairs - by expression in recombinant host cells with a secreting replicable genetic display package.

Example 46; Fig 52; 109pp; English.

The sequence is the light chain of clone MIF encoding an scFv fragment specific for both hen and turkey egg lysozyme (HEL and TEL). The DNA encoding the chain was amplified from a CDNA library prepd. from the spleen of an unimmunised mouse. The corresponding heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McCafferty J,
Jackson RH, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCCAfferty J, Pope AR, Johnson
Jackson RH, Holliger KP, Marks
Winter GP, Bonnert TP;
WPI; 92-056862/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R21310 stand
R21310;
21-MAY-1992
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Light chain of MIf clone.
Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coa pilus; g3p; binding; adsorption; gene VIII; diverse repertoire; specific binding pairs; replicable genetic display package.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region
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Sequence
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     84.0%;
larity 82.4%;
Conservative
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25..34
/label- CDR1
50..56
/label- CDR2
89..96
/label- CDR3
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Score 110; DB 4;
Pred. No. 3.49e-03;
2; Mismatches 1
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Pred. No. 3.49e-03;
2; Mismatches 1
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Clackson TP,
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                                                      Length 108
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Best Local
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20-MAR-1997.
13-SEP-1996; U14840.
14-SEP-1995; US-528104.
(REGC) UNIV CALIFORNIA.
(REGC) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           central nervous system spongiform encephalopathies in humans and animals. The scrapie isoform of the prion protein (Pr-Sc) is necessary for both the transmission and pathogenesis of the transmission end pathogenesis of the transmission end pathogenesis of the transmission and pathogenesis of the transmission and humans. The antibodies can be used in a method of the invention for detecting human Pr-Sc in a source. The antibodies specifically bind to prion proteins associated with disease and do not bind to denatured prp proteins not associated with disease. They can bind to prion proteins of a specific species of mammals. They can also have the ability to neutralise infectious prions. The antibodies can be used for screening for the presence of prions in products such as pharmaceuticals, food or cosmetics. They can also be used for prion neutralisation to purify products, for extraction of prion proteins or for therapy, for diseases such as bowine spongiform encephalopathy, creuzifeldt Jakob Disease, fatal familial insomnia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA.

Burton DR, Prusiner SB, Williamson RA;

WPI; 97-202357/18.

New antibodies to the scraple isoform of prion protein - used for detection of infectious prion proteins or for treating disease such as BSE, CJD or scraple Example 9; Fig 6; 99pp; English.

W18266-W18285 represent portions of the antibodies of the invention. The antibodies of the invention are able to bind the scraple isoform of prion protein PrP-Sc in situ. Prions are infectious pathogens that cause
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PrP 37 light chain variable region.

Prion protein: Prp: heavy chain variable region; antibody; scrapie;
Prion protein: Prp: heavy chain variable region; fatal familial insom
Light chain variable region; PrP-Sc; pathogen; fatal familial insom
central nervous system spongiform encephalopathy; human; therapy;
transmissible neurodegenerative disease; Creutzfeldt-Jakob Disease;
bovine spongiform encephalopathy; feline spongiform encephalopathy;
Serstmann-Strassler-Scheinker Disease.
25-MAY-1992 (first entry)
Sequence of the leader, variable region and first 16 AAs of the constant region of the kappa-chain (light chain) of MOPC41
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                                                                                                                             standard;
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14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109
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89..97
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57..88
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24..34
/note=
35..49
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98..109
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                                                                                                                             peptide;
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                                                                                                                                146
                                                                                                                                                                                                                                                                                                                                                        Score 110; DB 25;
Pred. No. 3.49e-03;
2; M1smatches 1
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atal familial insomnia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      feline spongiform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region
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Best Local
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(DNAX RES INST.
MOORE KW, Zaffaroni A;
WPI; 83-772290/39.
N-PSDB; N30165.
                                                                                                                                                                                   US534254-A.
09-JUL-1996.
06-FEB-1992; 1
06-FEB-1992; 1
07-OCT-1993; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAR-1983;
15-MAR-1982;
05-DEC-1983;
Compsis. Config. antigen-targetting antibody fragment construct comprising dimer of single-chain Fv fragments
Example 1; Columns 33-36; 30pp; English.
Variable heavy (VH) and variable light (VL) genes were cloned a 520C9 hybridoma cDNA library, using probes directed toward the antibody constant and joining regions. A two single chain Fv (a gene was constructed by connecting the VH and VL genes with a Ser rich polypeptide linker. The resulting 520C9 two sFv gene, which encodes the present sequence, was inserted into an expresent
                                                                                                                                                                                                                                                                                             29-OCT 1996 (first entry)
29-OCT 1996 (first entry)
520C9 anti-c-erbb-2 two single chain Fv construct.
520C9; anti-c-erbb-2 monoclonal antibody; single chain Fv; sFv; construct; polypeptide linker; C-terminal amino acid sequence; in vivo imaging; drug targetting experiment; homodimer; increased; binding avidity; tissue retention time.
                                                                                                                                (CHIR ) CHIRON CORP.
(CREA-) CREATIVE BIOMOLECULES INC.
HOUSTON LL. HUSTON JS, Oppermann
WPI: 96-333194/33.
                                                                                                                                                                                                                                                                                                                                                                                     W02280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Page 40-41; 68pp; English.

The pref. vector or plasmid of the invention has a double-stranded DNA seq. coding for a variable region of a light or heavy chain of IgG, or for a variable region of a light or heavy chain of an immunoglobulin specific for an enzyme or surface protein. The sequence esp. codes for a variable region of a light chain having 115 AAs or for a variable region of a heavy chain having the D region of the heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Кeу
                                                                                                                     N-PSDB; T36880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transformed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosis;
                                                                                                                                                                                                                                                                 peptide
                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n 84.0%;
Similarity 82.4%;
14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy; immunoglobulin.
                                                                                                                                                                                    : 831967.
: US-831967.
: US-133804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    001655.
US-358414.
US-558551.
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131..146
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23..130
                                                                                                                                                                                                                                                                  Location/Qualifiers 118..133
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                                                                                                                                                                                                                                                       /label-
                                                                                                                                                                                                                                                                                                                                                                                                Protein; 243 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 110; DB 4; Le
Pred. No. 3.49e-03;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid(s) .
for desired
                                                                                                                                               Η,
                                                                                                                                              Ring
                                                                                                         fragment constructs
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 expression
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                                                      the
                                       (SFV)
                                                                    from
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PF 0:
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                                                                                                                                                                                                                                                                                                                              antigon - for imaging or treating breast or ovarian cancer etc.

SC Claim 4; pages 60-61; 87pp; English.

C crebb-2 refers to a protein antigen expressed on the surface of tumour cells. Such as breast and ovarian tumour cells, which is an C approx. 200,000 mol. wt. acidic glycoprotein having an isolelectric pt. of about 5.3 (see 046083, R39569). A single chain FV (SFV)

C aper fusion including VH- and VL- encoding genes connected by a peptide encoding linker. Such linker sequences are set forth in linker sequences in R39572. Using 046084 for the 520C9 monoclonal antibody a single chain polypeptide can be produced having a binding affinity for a c-erbb-2 related antigen. 'X' in R39569 crefers to the location of a stop codon in 046084.
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Best Local S
Matches' 1
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Matches
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19-AUG-1993;
05-FEB-1993;
06-FEB-1992;
                                               WO9316185-A.
                                                            Synthetic.
                                                                         Tumour antigen; c-erbB-2; G-FIT
                                                                                           Sequence of G-FIT
                                                                                                            07-FEB-1994
                                                                                                                           R39571 standard; Protein; R39571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-1993;
05-FEB-1993;
06-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for imaging or treating breast or ovarian cancer etc.
                                                                                                                                                                                                                                      163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Houston LL, Huston WPI; 93-272889/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-FEB-1993; U01055.
06-FEB-1992; US-831967.
(CETU ) CETUS ONCOLOGY CORP.
(CREA-) CREATIVE BIOMOLECULES INC.
Houston LL, Huston JS, Oppermann H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-1994 (first entry)
Sequence of 520C9 sFv protein.
Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; biosynthetic single polypeptide chain binding site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; Q46084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vector, transformed into E. coli, and protein expression induced by the addn. of IPTG to the culture medium.

A compsn. comprising a carrier and the 2 sFv protein prod. can be used for in vivo inaging, and drug targetting experiments. The 2 sFv protein prod. is a homodimer, in which both fragments target the same antigen, therefore giving greater binding avidity and longer tissue retention times, compared to individual sFv protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R39569 standard;
R39569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9316185-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 gnsltwlqqepdgtikr 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 80.2%;
Local Similarity 82.4%;
                                                                                                                                                                                                                      gnsltwlqqepdgtikr 179
| :| ||||||||||
                                                                                                                                                                                                      GINLHWLQQEPDGTIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GINLHWLQQEPDGTIKR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fragments.
                                                                                                                                                                                                                                                                Similarity 82.4% 14; Conservative
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 246
                                                                                                                                                                                                                                                                             80.2%;
                                                                                                                                                                                                    66
                                                                                                                                      534
                                                                                                                                                                                                                                                        Score 105; DB 8; Len
Pred. No. 1.05e-02;
Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 105; DB 18;
Pred. No. 1.05e-02;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ring
                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                        0
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RESULT ACC RESULT TO THE RESULT ACC RESULT A
DR WPI; 94-12030/15.

PT Method of resurfacing of rodent antibodies to produce humanised PT antibody forms - for producing non-human antibodies with improved PT antibody forms - for producing non-human antibodies with improved PT therapeutic efficiency by presenting human surface on V-region CC Example 1; Fig 3A; 230pp; English.

CC The present sequence is that of the light chain variable (LC VR) region CC antibody glb2. This sequence was aligned with 11 other known CC acid residues was determined. This information can be used in a method to CC determine how to modify a rodent antibody or fragment by resurfacing in CC alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 63, 66, 73, 86, CC combinations of surface residues in the marine sequences were found in CC the human sequences and vice versa. However the residues in individual Sc Sequence 109 AA;
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Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                 (IMMU-) IMMUNOGEN INC.
Guild BC, Pedersen JT,
WPI; 94-120230/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-APR-1994.
07-SEP-1993; 307051.
09-SEP-1992; US-942245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Light chain variable region of murine antibody glb2. antibody; humanised; murine; human; heavy chain; light; variable; framework region; complementarity determining region; reshaping; modelling; surface residue; modify.
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R52030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c-erabs-2 refers to a protein antigen expressed on the surface of tumour cells, such as breast and ovarian tumour cells, which is approx. 200,000 mol. wt. acidic glycoprotein having an isolelect pt. of about 5.3 (see Q46083, R39568).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Houston LL, Husto WPI; 93-272889/34. N-PSDB; Q46086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 gnsltwlsgepdgtikr 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CETU ) CETUS ONCOLOGY CORP
(CREA-) CREATIVE BIOMOLECULI
Houston LL, Huston JS, Opp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 GINLHWLQQEPDGTIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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llarity 76.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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/label= CDR_2
57..88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "CDR 1
35..49
/label= FR_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label- FR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= framework_region_1
/note= "FR 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=_complementarity_determining_region_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complementarity determining region; e residue; modify.
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Pred. No. 7.41e-02
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          æ
                                                                                                                                                                                                                                                                                                                                                                                                                                 Roguska
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R79247 standard; 1
R79247;
21-DEC-1995 (fir:
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30-MAR-1994;
30-MAR-1994;
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Light chain; RT3; murin-
pattern A
 synthetic.
wo9520607-A.
03-AUG-1995.
                                                                                                                                                                                                      T04625 encodes R80078 mouse derived light chain RT3 phage antibody. The DNA was used in the prepn. of catalytic antibody (CA) producing bacteriophage. The CAs can be used to activate/deactivate a biological function in an animal by enhancing the rate of cleavage, or formation of a specific bond within a mol. in vivo. Sequence 90 AA;
                                  Monoclonal antibody; heavy metal; mercurv:
                                                                                                                                                                                                                                                                                      Production of catalytic antibodies displayed on phage - by
generating a gene library of antibody-derived domains and expressing
                                                                                                                                                                                                                                                                                                            WPI; 95-358624/46.
N-PSDB; T04625.
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Chiswell D, Dars
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                             light chain.
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Disclosure; Fig 9;
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Similarity 76.5%;
13; Conservative
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larity 85.7%;
Conservative
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27..40
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41..47
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89..90
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79..88
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48..78
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16..26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 90
                                                                                Protein; 107
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inal fragment"
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                                                                                                                                                                                                                                                                                                                                Fitzgerald K, Kenten JH;
Smith RG, Titmas RC, Williams
                                                                                                                                                                Score 93; DB 16;
Pred. No. 1.41e-01;
2; Mismatches 1
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1. No. 1.14e-01;
Mismatches 2
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antibody; bacteriophage;
                                                  antibody 1F10
                                         variable
                                                                                                                                                                                   Length 90
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Best Local S
Matches 1
                                                                                                                                                                                                                                                                     Synthetic.
w09520607-A.
03-AUG-1995.
27-JAN-1995; U01199.
27-JAN-1994; US-187407.
27-JAN-1994; US-187407.
LOPEZ O, Wagner EW, Wyl
WPI; 95-275415/36.
New polypeptide(s) which bind heavy metals, esp. mercury - deriver monoclonal antibodies, used for detecting, removing, adding or neutralising heavy metals
Claim 23; Page 70; 106pp; English.

Hybridoma antibodies have been produced with the spleen cells of BALB/c mouse that had received multiple injections of mercuric ion reacted with glutathione to produce a mercuric ion coordinate covalent compound which was covalently bound to keyhole limpet hemocyanin (KiH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 15B6 and 3E8) were producing MAbs that were strongly positive against glutatione-mercuric ions but negative against glutathione without mercuric ions. RNA was isolated from hybridoma cells with
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Lopez O, Wagner FW,
WPI; 95-275415/36.
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27-JAN-1994;
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US-187407
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1. No. 1.41e-01;
Mismatches 3;
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Hybridoma antibodies have been produced with the spleen cells of covalent compound which was covalently bound to keyhole limpet the memoryanin (KLH). Eight hybridomas (IFIO, 4AIO, ICII, 504, 31F8, 2D5, CC against galtatione-mercuric ions but negative against glutatione-mercuric ions but negative against glutatione-mercuric ions but negative against glutatione-mercuric ions but negative against glutatione (CC without mercuric ions. RNA was isolated from hybridoma cells with CC guanidine isothlocyanate. First strand cDNA synthesis was catalysed CC were complementary to the 5' end of the CHI domain of the heavy CC that C kappa domain. Some of the primers used for cDNA synthesis are CC shown in 097511-097518. The primer used for cDNA synthesis are CC wariable region of a particular antibody polypeptide was also used CC variable region of a particular antibody polypeptide was also used CC was used to amplify the mAb 2D5 and 58 heavy chains. The sequences CC m 197498-097510 and the deduçed AA sequences in R79241-R79250 c and in the claims are different from the descriptions in the CC and in the claims are different from the descriptions in the CC and in the claims are different from the descriptions in the CC cand in the claims are different from the descriptions in the CC cand in the claims are different from the descriptions in the CC cand in the claims are different from the descriptions in the CC cand in the claims are different from the descriptions in the conditions of the conditions in the claims are different from the descriptions in the claims are different from the 
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Best Local
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Claim 23; Page 66; 106pp; English.
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Lopez O, Wagner FW, W
WPI; 95-275415/36.
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27-JAN-1995; U01199.
27-JAN-1994; US-187407
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Monoclonal antibody; heavy metal; mercury; variable region;
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llarity 70.6%;
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descriptions in the sequence
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Pred. No. 1.41e-01;
2; Mismatches 3;
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D-X-G-X-X motif "

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RESULT
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AC R2
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                                                                                                                                                                                                                                                                                                                            pilus; g3p; bindi
specific binding
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R21286;
21-MAY-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   Murine VL kappa
Fd; bacteriophaq
                                                                                                                                                                                                                 binding_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells (APC), genetically modified to contain at least one antigen presenting exclusively at one or more presented to contain at least one antigen cells (APC), genetically modified to contain at least one antigen exclusively at one or more preselected sites. The conjugate is capable of delivering the antigen to APC and eliciting an immune response to the antigen. The new conjugates are useful as vaccines and are able in a specific example, a conjugate was constructed using the murine anti-human class II monoclonal antibody secreted by hybridoma at andemly linked T and B cell epitope derived from HIV MN strain. The present sequence represents the light chain variable region antigen CLTB36 was used in the preparation of a conjugate with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immuno:diagnosis

Example 1; Fig 1A; 64pp; English.

Example 1; Fig 1A; 64pp; English.

Movel recombinant conjugate antibody molecules comprise a monoclonal antibody specific for a surface structure of antigen presenting antibody specific for a surface structure of antigen presenting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant conjugate antibody mol., modified for delivering an antigen - elicits enhanced immune response without the use of adjuvant to generate antibodies which are useful in vaccines or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CONN-) CONNAUGHT LAB
Anand NN, Barber BH,
WPI; 97-077271/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; T77851.
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07-JUN-1995;
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Antibody; light chain; variable region; hybridoma cell line 44H104;
immune response; enhance; stimulate; vaccine; immunodiagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 ltwlqqkpdgtikr 68
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Murine anti-human class
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                                                                                                                                                                                                                                                                                                    ine VL kappa group v chain "a", specific for phox.
bacteriophage; gene III; filamentous; phagemid; capsid; coat;
us; g3p; binding; adsorption; gene VIII; diverse repertoire;
cific binding pairs; replicable genetic display package.
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larity 85.7%;
Conservative
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89..96
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50..56
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2; Mismatches 3;
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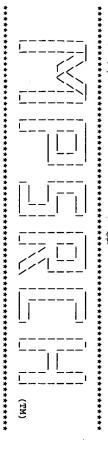
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PN W09201047-A.
PP 10-JUL-1991; G01134.
PR 10-JUL-1990; GB-015198.
PR 10-JUL-1990; GB-015198.
PR 19-OCT-1990; GB-012845.
PR 19-OCT-1990; GB-012845.
PR 19-OCT-1990; GB-02845.
PR 19-OCT-1990; GB-02845.
PR 11-MOV-1990; GB-024503.
PR 06-JMAR-1991; GB-010549.
PA (CAMB-) CAMBRIDGE ANTIBODY.
PA (KEDI-) MED RES COUNCIL.
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Wilter GP, Bonnert TP;
PI Wilter GP, Bonnert TP;
PR WPT: 92-056862/07.
PT recombinant host cells with a secreting replicable genetic display package.
PS Example 21; Fig 24; 209pp; English.
PT recombinant host cells with a secreting replicable genetic from a single chain FV library from an immunised mouse. The librar Trom marks from mice immunised with phox coupled to chicked serum captured from a single chain FV library from an immunised with gene LI. The result-cing library of clones were sequenced revealing eight different VH genes (A-H) (see C23447-84) and ligated into fdCAPZ (see C23445) for exclones were sequenced revealing eight different VH genes (A-H) (see C1264-71) in a variety of pairings with the seven different Vk c genes (a-g). Of the twenty three clones sequenced three were of clones were NF-d combinations. The Kd of VH-By/K-d for phox-GABA was 10 mk. Only two other combinations (of eleven tested) were combinations of eleven tested) were combinations (of eleven tested) were combined were combined with antigen, probable combined with antigen, probable combined with antigen, probable combined were combined with antigen, probable combined with antigen, pr
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Search completed: Tue Apr 20 13:59:29 1999 Job time : 16 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. n on: Tue Apr 20 13:58:42 1999; MasPar time 3.59 Seconds 177.483 Million cell updates/sec

Sequence: Description: Perfect Score: Title: >US-08-836-455-2 (50-66) from US08836455.pep (2 of 3) 1 GINLHWLQQEPDGTIKR 17

Scoring table: PAM 150 Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir58 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 28.231; Variance 51.804; scale 0.545

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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à	76	76	76	76	76	76	76	76	76	76	76	84	84	90	91	91	94	94	110	110	110	110	Score
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100	107	107	107	107	107	107	107	107	107	105	93	101	101	92	108	91	106	98	130	106	106	88	Length
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Ty Nappa	Ig kappa			Ig light			Ig kappa					kar	kar	kar	nitrophe	kar	kar			Ig kappa		Ig kappa	Descripti
	kappa	kappa	kappa						kappa cha	kappa		kar	kar	kar	frot	kar	kar	Ig light chain	kappa			Ig kappa chain	Description
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1.94e-01	4e-	1.94e-01	1.35e-01	Se-	Še	1.35e-01	1.35e-01	1.35e-01	1.35e-01	1.35e-01	ē	1.35e-01	.35e-		.35e-						

ALIGNMENTS

RESULT ENTRY

Qy RESULT RESULT TILE ORGANI DATE ACCESS REFERE	Ma Ma	5 E A 1 - 5 E A	CLAS	** *	REFE	ENTRY TITLE ORGANI DATE ACCESS
ISM ISM		1.05 6-16 17-31 32-38 39-70 71-79 80-88	##molecule_type mRNA 1-88 ##residues 1-88 CLASSIFICATION #superfam KEYWORDS heterotet	#title #cross-referent #accession	REFERENCE #authors #journal	ENTRY TITLE ORGANISM DATE ACCESSIONS
:	84 82 rvat	#region framework 1\ #region complementarity-determining 1\ #region framework 2\ #region complementarity-determining 2\ #region framework 3\ #region framework 4\ #region framework 4 #length 88 #checksum 7092	_type mRNA 1-88 ##label SHL #superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin	Anti-DNA antibodies from autoimmune mice arise by cional expansion and somatic mutation. cross-references MUID:90111618 accession PLO261		PL0261 #type fragment Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment) #formal_name Mus musculus #common_name house mouse 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997 PL0261

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TITLE
CONTAINS
ORGANISM
DATE
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35-49
50-56
57-88
89-97
98-106
SUMMARY
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ENTRY
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ENTRY
TITLE
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1 - 23
24 - 34
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57 - 88
89 - 97
98 - 106
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#Cross-references MUID:90111618
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                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA #residues 1-106 ##label SHL FIGATION #superfamily immunoglobulin V region; immunoglobulin
                                                                                                                               50
                                                                                                                                         30 GRSLNWLQQEPDGTIKR 46
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Local Similarity 82.4%;
                                                                                                                            GINLHWLQQEPDGTIKR 66
                                                                                                                                                                                                    Similarity 82.4%;
KVMSM4 #type complete
I9 kappa chain precursor V region (MOPC 41) - mouse
I9 kappa chain precursor V region VK41
#formal_name Mus musculus #common_name house mouse
24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change
                                                                                                                                                                                                                                               #length 106
                                                                                                                                                                                                                                                                                                                                                                        heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shlomchik, M.; Mascelli, M.; Shan, H.; Ra
D.; Marshak-Rothstein, A.; Weigert, M.
J. Exp. Med. (1990) 171:265-297
Anti-DNA antibodies from autoimmune mice
                                                                                                                                                                                                                                                                                                                                                                                                                                          PL0259
                                                                                                                                                                                     Conservative
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If kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
16.5ep-1992 #sequence_revision 16.5ep-1992 #text_change
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#length 106
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J. Exp. Med. (1990) 171:265-297
Anti-DNA antibodies from autoimmune mice arise by expansion and somatic mutation.
nces MUID:90111618
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framework 3\
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framework 4
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framework 3\
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Pred. No. 2.15e-07;
2; Mismatches 1
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Pred. No. 2.15e-07;
2; Mismatches 1;
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#journal
#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Burstein, Y.; Schechter, I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720
#title Amino acid sequence of the NH-2-terminal extra piece segments of the precursors of mouse immunoglobulin lambda-1-type and #cross-references MUID:77148916
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#journal Nature (1979) 280:370-375
#title A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.
#cross-references MUID:79221900
#accession A93211
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##residues 23-49', 8',51-53,'LSB',57-58,'ZZ',61-62,'BZ',65-76,'B'
78-108,110-130 ##label GRA
                                                                                                                                                                         52 GSSLNWLQQEPDGTIKR 68
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                                                                                                                                             GINLHWLQQEPDGTIKR 66
                                                                                                                                                                                                                                                  h 84.0%;
Similarity 82.4%;
PH1062 *type fragment
If light chain V region (clone 202.105) - mouse (fi
#formal_name Mus musculus *common_name house mouse
                                                                                                                                                                                                                                                                                                       #product Ig kappa chain V region (MOPC 41) #status
experimental #label M41\
#domain immunoglobulin homology #label IMM\
#disulfide_bonds #status predicted
#length 130 #molecular-weight 14311 #checksum 6707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heav (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
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A93211; B93211; A93815; A94239; A01922; A01923
A93211
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1-33 ##label BUR
Met-3 is apparently used as an alternative initiator
25% of the chains
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Pred. No. 2.15e-07;
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ORGANISM

mouse (fragment)

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CLASSIFICATION
KEYWORDS
FEATURE
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24-34
35-49
50-56
57-88
89-97
98-106
                                                                  RESULT
ENTRY
TITLE
ORGANISM
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FICATION #superfamily immunoglobulin V region; 1
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##residues 1-98
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Similarity 85.7%;
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Similarity 85.7%;
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D.; Marshak-Rothstein, A.; Weigert, M.
J. Exp. Med. (1990) 171:265-297
Anti-DNA antibodies from autoimmune mice
expansion and somatic mutation.
         S17622 *type complete
Ig kappa chain V region - mouse
#formal_name Mus musculus #common_name house
22-Nov-1993 #sequence_revision 10-Nov-1995 #t
09-May-1997
S17622
S17623
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Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
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#length 98 #cl
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Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1
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#region framework 2\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Lesley, S.A.; Patten, P.A.; Schultz, #journal Proc. Natl. Acad. Sci. U.S.A. (1993) #title A genetic approach to the generation enhanced catalytic activities. #cross-references_MUID:93165660
#journal EMBO J. (1985) 4:3681-3688

The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded (anti-idiotypic) antibodies in the GAT system.

#cross-references_MUID:86136012
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                                                                                                       #authors
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##molecule_type nucleic acid
##residues 1-91 ##label CLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##note
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Similarity 85.7%;
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Similarity 78.6%;
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heterotetramer; immunoglobulin
#length 91 #molecular-weight 9895 #checksum 3446
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A47271
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Mus musculus (house mouse) gene engineered and expressed
Escherichia coli
                                                                                                     Ollier, P.; Rocca-Serra, J.;
                                                                                                                                                                     D28840 #type fragment
Ig kappa canain V region (HP29) - mouse (fragment)
Ig kappa canain V region (HP29) - mouse house mouse
#formal_name Mus musculus #common_name house mouse
29_Aug-1987_#sequence_revision 29-Aug-1987 #text_change
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#length 108 #checksum 9036
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NCBIP:124859)
parts of this sequence were determined by protein
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Pred. No. 4.70e-04
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Pred. No. 4.70e-04;
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) 90:1160-1165
n of antibodies :
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Matches 1
                                                                                                                             regulation of a germ-line network by paucigene encoded (anti-idiotypic) antibodies in the GAT system.

#accession C28840
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The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encode (anti-idiotypic) antibodies in the GAT system.

#cross-references MUID:86136012
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##molecule_type mRNA
##residues 1-101 ##label OLL
#Fresidues 1-101 #munoglobulin V region;
heterotetramer; immunoglobulin
heterotetramer; immunoglobulin
heterotetramer; immunoglobulin
heterotetramer; immunoglobulin
                                                                                                             ##residues
                                                                                                                       ##molecule_type mRNA
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##residues 1.92 ##label OLL
##cross-references GB:X03384; NID:g52157; PID:g52158
##CIGATION #superfamily immunoglobulin V region; immuDS
heterotetramer; immunoglobulin
kDS heterotetramer; immunoglobulin
#length 92 #checksum 7017
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    Similarity
10; Conse
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Similarity 58.8%;
10; Conservative
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A91028
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Ig kappa chain V region (HP22) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change
16-Aug-1996
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Ig kappa chain V region (HP27) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
29-Aug-1987 #sequence_revision 29-Aug-1987 #text_.
16-Aug-1996
                                                             #length
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                64.1%;
58.8%;
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                                                             #checksum 5983
 Score 84; DB 2; I
Pred. No. 6.97e-03;
4; Mismatches 3
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Pred. No. 6.97e-03;
4; Mismatches
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                                                                                                                                                                                                                                                 J.; Somme,
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##cross references EMBL:X75105; NID:g414153; PID:g414154
CLASSIFICATION #superfamily immunoglobulin V region; immunog
KEYWORDS immunoglobulin
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*accession PH0087
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##cross-references GB:X57639; NID:g296839; PID:g296840
##CICATION #superfamily immunoglobulin V region; immunoglobulin beterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                 ##molecule_type mRNA
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 53
                           33 LNWYQQKPDGTVK 45
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LHWLQQEPDGTIK
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Similarity 69.2%;
9; Conservation
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Analysis of the structural diversity of monoclonal antibodi
                                                                                                                         #length
                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Mus musculus #common_name house mouse 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change
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S38559
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If kappa chain V region (ASWU1) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
20-Mar-1998
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Ig kappa chain V region (anti-cyclosporin C
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fregion complementarity-determining
fregion complementarity-determining
fregion complementarity-determining
fth 105 #checksum 9783
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Pred. No. :
2; Mismai
                                                          Score 76; DB 2;
Pred. No. 1.35e-01
2; Mismatches
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CLASSIFICATION #superfam
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Matches 9; Conservative
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#superfamily immunoglobulin; V region; immunoglobulin homology
immunoglobulin
#length 107 #checksum 9096
                                                                                                                                                                                                                                                                                                                                                      Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C.A.; Capra, J.D.; Meek, K. Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9508-9512 Molecular characterization of monoclonal CRI-A-positive anti-arsonate antibodies derived from idiotype-negative mice bearing a light chain polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B48677 #type fragment
Ig kappa chain V-J region (44.1) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
19-May-1994 #sequence_revision 19-May-1994 #text_change
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#formal_name Mus musculus #common_name house mouse
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Pred. No. 1.35e-01;
2; Mismatches 2
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Pred. No. 1.35e-01;
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm on:

n on: Tue Apr 20 14:04:22 1999; MasPar time 2.65 Seconds 67.085 Million cell updates/sec

Title: >US-08-836-455-1_1
Description: (24-34) from trans.pep (1 of 3)
Perfect Score: 63
Sequence: 1 MTQSPSSLSAS 11
Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 15.144; Variance 52.220; scale 0.290

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	18	17	16	15	14	13	12	11	10	9	8	7	6	ر ن	4	ω	2	_	Result	
	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	Score	
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-	Huma	Anti-TNF-alpha antibo	Light chain variable	Chimeric humanised	Anti-CEA antibody	Anti-CEA antibody	Humanised alpha-4	Antibody LD1-117-V	Antibody LD2-5-VL	Antibody LD1-52-VL	Antibody LD1-40-VI	Antibody LD2-14-VI	Antibody LD2-20-VI	Antibody LD1-110-VL	Antibody LD1/2-6-3	Antibody LD1-6-17-VL	Antibody LD1-84-VL	Antibody LD2-4-VL	Description	
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Query Match 100.0%; Best Local Similarity 100.0%; Matches 11; Conservative

Score 63; DB 29; Length 104; Pred. No. 3.52e+00; 0; Mismatches 0; Indels

0

Gaps

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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19
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R. pipiens recombinan	Humanised anti-CD38 m	Chimeric humanised Mu	Human anti-RSV monocl	Humanised antibody 80	Humanised light chain	ant	Light chain of full 1	chain of h		Humanised anti-VLA-4	Chimaeric human/murin	Human/murine chimeric		Human/murine chimeric	Human/murine chimeric	Human/murine chimeric	Humanised light chain	Human vkappa65.15 fra	Interleukin-5 humanis	Light chain variable	Variant variable ligh	hWI2 light chain.	light	119	Light chain variable	Light chain variable
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W09749809-A1.

31-DEC-1997.

20-JUN-1997; E03253.

20-JUN-1997; E03253.

R 24-JUN-1996; EP-810421.

ROTK-) ROTKREUZSTIFTUNG ZENT LAB BI
(ROTK-) ROTKREUZSTIFTUNG ZENT LAB BI
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CC polypeptide of the invention The polypeptides are capable of forming CC antigen binding structures with specificity for Rhesus D antigens which CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of CC variable heavy (VH) and variable light (VL) chain sequences. The CC variable heavy (VH) and variable light (VL) chain sequences. The CC include Rhesus D antigens which would benefit from anti-Rhesus D immunoglobulin, CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the CC protection of Rhesus negative women before or immediately after the birth of a Rhesus positive child to prevent haemolytic disease of the newborn immunoglobulin can be used after mistransfusions of Rhesus positive blood to Rhesus negative recipients in order to prevent sensitisation to the Rhesus D antigen. The products can also be used as diagnostic reagents.

Sequence 105 AA;
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New Rhesus D antigen binding Rhesus D antigen in therapy, thrombocytopenic purpura
                                                                                                      WPI; 98-077173/07.
N-PSDB; V19763.
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Antibody LD1-6-17-VL chain sequence.
Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
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12-JUN-1998 (first entry)
Antibody LD1-84-VL chain sequence.
Antibody: variable heavy chain; VH chain; variable light chain; VL chain;
Antibody: variable heavy chain; VH chain; variable light chain; VL chain;
Antibody: variable heavy chain; VH chain; variable light chain; VL chain;
Antibody: variable heavy chain; VH chain; herapy;

Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;

Alexander of the newborn.
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20-JUN-1997; E03253.
24-JUN-1996; EP-810421.
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Amstutz H, Imboden M, Miescher S, Morell A, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W52217 standard;
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Similarity 100.0%;
11; Conservative
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Pred. No. 3.52e+00;
0; Mismatches 0;
                              poly:peptide(s) -
e.g. for treating
                                                                                                                                                                                  BLUTSPENDE.
Morell A, Stadler
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                              used to neutralise idiopathic
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100.0%; llarity 100.0%; Conservative

Score 63; Pred. No. 0; Misma

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DB 29; 1

Length 105;

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FRESULT ACCORDED TO THE STATE OF THE STATE O
New Rhesus D antigen binding poly:peptide(s) - used to neutralise PT New Rhesus D antigen in therapy, e.g. for treating idiopathic thrombocytopenic purpura
PS Claim 1; Fig 15B; 68pp; English.
CC This sequence is the antibody LDL/2-6-3-VL chain sequence, which is a CC polypeptide of the invention. The polypeptides are capable of forming CC antigen binding structures with specificity for Rhesus D antigens which CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of CC variable heavy (VH) and variable light (VL) chain sequences. The CC antibodies are active against the Rhesus D antigen. They can be used for treating disorders which would benefit from anti-Rhesus D immunoglobulin, CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the protection of Rhesus negative women before or immediately after the birth CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D in subsequent pregnancies. In addition, anti-Rhesus D continuoglobulin can be used after mistransfusions of Rhesus positive blood CC Rhesus D antigen: The products can also be used as diagnostic reagents.
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CC This sequence is the antibody LD1-6-17-VL chain sequence, which is a CC polypeptide of the invention. The polypeptides are capable of forming CC antigen binding structures with specificity for Rhesus D antigens which include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of CC variable heavy (VH) and variable light (VL) chain sequences. The CC antibodies are active against the Rhesus D antigen. They can be used for treating disorders which would benefit from anti-Rhesus D immunoglobulin, CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the protection of Rhesus negative women before or immediately after the birth CC of a Rhesus positive child to prevent haemolytic disease of the newborn CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D immunoglobulin can be used after mistransfusions of Rhesus positive blood to Rhesus D antigen. The products can also be used as diagnostic reagents.

CC Rhesus D antigen. The products can also be used as diagnostic reagents.
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Best Local
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31-DEC-1997; E03253.
20-JUN-1997; E03253.
24-JUN-1996; EP-810421.
(ROTK-) ROTKREUZSTIFTUNG ZENT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPĬ; 98-077173/07.
N-PSDB; V19765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody LD1/2-6-3-VL chain sequence.
Antibody; variable heavy chain; VH chain; variable light chain; VL chain; Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy; idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vogel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W52241 standard; Protein; 105 W52241;
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Similarity 100.0%;
11; Conservative
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Pred. No. 3.
0; Mismatc
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3.52e+00;
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ase of the newborn.
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CC laim 1; Fig 4B; 68pp; English.

CC This sequence is the antibody LD1-110-VL chain sequence, which is a CC polypeptide of the invention. The polypeptides are capable of forming CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of CC variable heavy (VH) and variable light (VL) chain sequences. The CC antibodies are active against the Rhesus D antigen. They can be used for CC treating disorders which would benefit from anti-Rhesus D immunoglobulin, CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the CC protection of Rhesus negative women before or immediately after the birth CC of a Rhesus positive child to prevent haemolytic disease of the newborn CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D cC immunoglobulin can be used after mistransfusions of Rhesus positive blood CC Rhesus D antigen. The products can also be used as diagnostic reagents.

CC cannence 105 Ah.
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Best Local S
Matches 1
New Rhesus D antigen binding poly:peptide(s) - used to neutralise Rhesus D antigen in therapy, e.g. for treating idiopathic thrombocytopenic purpura
Claim 1; Fig 13B; 68pp; English.
This sequence is the antibody LD2-20 VL chain sequence, which is a polypeptide of the invention. The polypeptides are capable of forming antigen binding structures with specificity for Rhesus D antigens which include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
                                                                                                                                                                                                     31-DEC-1997.
31-DEC-1997; E03253.
20-JUN-1996; EP-810421.
24-JUN-1996; EP-810421.
(ROTK-) ROTKREUZSTIFTUNG ZENT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUN-1997; E03253.
24-JUN-1996; EP-810421.
(ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
Amstutz H, Imboden M, Miescher S, Morell A, S
Vogel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody LD1-110-VL chain sequence.

Antibody; variable heavy chain; VH chain; variable light chain; VL chain Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy; idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
                                                                                                                                                                                                                                                                                                                             Antibody LD2-20-VL chain sequence.

Antibody; variable heavy chain; VH chain; variable light chain; VL chain; Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy; idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Rhesus D antigen binding Rhesus D antigen in therapy,
                                                                                                                                                         N-PSDB; V19761.
                                                                                                                                                                                                                                                                                                                                                                                                                                             W52237 standard; Protein; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhesus D antigen.
Sequence 105 AA;
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N-PSDB; V19743.
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WO9749809-A1.
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W52219 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 MTQSPSSLSAS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 mtqspsslsas 12
                                                                                                                                                                     98-077173/07.
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Similarity 100.0%;
11; Conservative
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Pred. No.
0; Misma
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e.g. for treating idiopathic
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3.52e+00;
1.3.52e+00;
                                                                                                                                                                                                   A,
       for Rhesus D antigens which CDR 3 regions of pairs of
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1.5

RESULT
ID WI
AC WI
DT 1:

W52213;

12-JUN-1998 (first Antibody LD1-40-VL W52213 standard;

(first entry)

sequence

Protein; 106

δõ 밁

24

MTQSPSSLSAS 34

2 mtqspsslsas 12

Query Match Best Local Matches

h 100.0%; Similarity 100.0%; 11; Conservative

Score 63; DB 29; Pred. No. 3.52e+00; 0; Mismatches C

0

Indels

0;

Gaps

0

Length 105;

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PT thrombocytopenic purpura

PS Claim 1; Fig 11B; 68pp; English.

CC This sequence is the antibody LD2-14-VL chain sequence, which is a CC polypeptide of the invention. The polypeptides are capable of forming CC antigen binding structures with specificity for Rhesus D antigens which include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of CC variable heavy (VH) and variable light (VL) chain sequences. The CC antibodies are active against the Rhesus D antigens. They can be used for treating disorders which would benefit from anti-Rhesus D immunoglobulin, CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the protection of Rhesus negative women before or immediately after the birth CC of a Rhesus positive child to prevent haemolytic disease of the newborn CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D content of the Rhesus D segative recipients in order to prevent sensitiation to the phesus D antigen. The products can also be used as diagnostic reagents.
                      RESULTANT PROCESS OF THE STATE 
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Best Local S
Matches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Rhesus D antigen binding poly:peptide(s) - Rhesus D antigen in therapy, e.g. for treating
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N-PSDB; V19757.
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20-JUN-1997;
24-JUN-1996;
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WO9749809-A1.
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1996; EP-810421.
ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
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Similarity 100.0%;
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Pred. No. 3.52e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used to neutralise idiopathic
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RESULT
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New Rhesus D antigen binding poly:peptide(s) - used to neutralise Rhesus D antigen in therapy, e.g. for treating idiopathic thrombocytopenic purpura Claim 1; Fig 2B; 6Bpp; English.

This sequence is the antibody LD1-52-VL chain sequence, which is a polypeptide of the invention. The polypeptides are capable of forming antigen binding structures with specificity for Rhesus D antigens which include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of variable heavy (VH) and variable light (VL) chain sequences. The antibodies are active against the Rhesus D antigen. They can be used for treating disorders which would benefit from anti-Rhesus D immunoglobulin, e.g. idiopathic thrombocytopenic purpura. They can also be used for the protection of Rhesus negative women before or immediately after the birth
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Antibody; variable heavy chain; VH chain; variable light chain; VL chain; Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy; idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
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N-PSDB; V19739.
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24-JUN-1996; EP-810421.
(RÖTK-) ROTKREUTSTIFTUNG ZENT LAB BLUTSPENDE.
Amstutz H, Imboden M, Miescher S, Morell A, Stadler
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WO9749809-A1.
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Rhesus D antigen in therapy, e.g. for treating idiopathic
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N-PSDB: V19737.
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24-JUN-1996; EP-810421.
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Sequence 106 AA
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Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
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H, Imboden M, Miescher S,
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Claim 1; Fig 8B; 68pp; English.

CC This sequence is the antibody LD2-5-VL chain sequence, which is a complete sequence is the antibody LD2-5-VL chain sequence, which is a complete sequence is the antibody LD2-5-VL chain sequence, which is a complete sequence is the invention. The polypeptides are capable of forming complete binding structures with specificity for Rhesus D antigens which can be used for the complete sequence of the invention of Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of complete complete sequences and complete sequences. The complete sequence of the sequences of the complete sequence of the complete sequence of the complete sequence of the complete sequence of the sequence of the complete sequence could be complete sequence of the newborn of a Rhesus positive child to prevent haemolytic disease of the newborn (HDN) in subsequent pregnancies. In addition, anti-Rhesus D introduction can be used after mistransfusions of Rhesus positive blood to Rhesus negative recipients in order to prevent sensitisation to the Rhesus D antigen. The products can also be used as diagnostic reagents. Sequence 106 AA;
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W09749809-A1.
31-DEC-1997.
20-JUN-1997; E03253.
20-JUN-1996; EP-810421.
24-JUN-1996; EP-810421.
CROTK-) ROTKREDESTIFTUNG ZENT LAB BLUTSPENDE.
CROTK-) ROTK-BLUTSPENDE.
                                                                                                       W5221 standard; Protein; 106 AA.
W52221;
12-JUN-1998 (first entry)
Antibody LD1-117-VL chain sequence.
Antibody; variable heavy chain; VL chain; variable light chain; VL chain; Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy; idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
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W52227 standard; Protein; 106

W52227;

12-JUN-1998 (first entry)
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Antibody; variable heavy chain; VH chain; variable light chain Antibody; variable heavy chain; VH chain; HDN; therapy; Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy; idiopathic thrombocytopenic purpura; haemolytic disease of the interpretable of the chain and t
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Pred. No. 3.52e+00;
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RESULT WZ AC OX DE HI KW AI KW M M KW M M KW A A KW A K
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This sequence is the antibody LD1-117-VL chain sequence, which is a
polypeptide of the invention. The polypeptides are capable of forming
antigen binding structures with specificity for Rhesus D antigens which
cinclude Rhesus D-specific CDR 1, CDB 2, and CDR 3 regions of pairs of
cvariable heavy (VH) and variable light (VL) chain sequences. The
creating disorders which would benefit from anti-Rhesus D immunoglobulin,
c. e.g. idiopathic thrombocytopenic purpura. They can also be used for
the protection of Rhesus negative women before or immediately after the birth
of a Rhesus positive child to prevent haemolytic disease of the newborn
(HDN) in subsequent pregnancies. In addition, anti-Rhesus D solitive blood
to Rhesus negative recipients in order to prevent sensitisation to the
Rhesus D antigen. The products can also be used as diagnostic reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised alpha-4 integrin antibody 21.6 VL La. Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
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W22412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-DEC-1997.
20-JUN-1997; E03253
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROTKREUZSTIFTUNG ZENT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetic
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35..49
/label= FR2
                                                                                                                                                                                              21.6 VL, ir
CDR2 loop"
                             /note=
57..88
                                                                                                                                                                                                                                                                /note- "REI framework region 45
                                                                                                                                                                                                                                                                                                                                                                                                           /note= "REI framework region 24..34
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                                                                                                                      21.6 VL,
                                                                                                                                                                                                               /note= "REI Lys-45
21.6 VL, important
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                                                                            /label- CDR2
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                                                                                                                           located
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Pred. No. 3.52e+00;
0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                poly:peptide(s) - used to neutralise
e.g. for treating idiopathic
                                                   complementarity
                                                                                                                                                                                                                                                                                                                                                            complementarity determining region
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This polypeptide, designated La, comprises the light chain variable region (VI) of a humanised alpha-4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VI region (see W22409) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human REI framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate fragments of mouse and human DNA sequences. The humanised 21.6 VL and a humanised 21.6 VH (see W22413) can be used to produce a claimed humanised 21.6 vH (see W22413) can be used to produce a claimed humanised 21.6 treating asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibody has a half-life in the human circulation essentially equivalent to that to sequence 106 AA:
                                                                                                                                                                                                      Query Match
Best Local S
Matches 1
                                                                                W41390;
W41390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_difference
                        02-JUN-1998 (first entry)
Anti-CEA antibody light chain variable region VK4.
Anti-CEA antibody; carcinoembryonic antigen; 806.077
Cancer diagnosis; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_difference
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 Synthetic.
W09742329-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bendig MM, Jones ST, Leger OJ, Saldanha WPI; 97-297879/27.
Uses of humanised alpha-4 integrin antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_difference
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29-MAY-1997.
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21-NOV-1995; US-561
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                                                                                             standard; Protein; 107
                                                                                                                                                                                                        11;
                                                                                                                                                                                                                    Similarity
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llarity 100.0%;
Conservative
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/note= "21.6
97..106
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21.6 VL, important
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of human kappa light chain o
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3.52e+00;
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                            region;
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the CDR2
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Matches 1
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Copley CG, Edge MD, Emery SC;

WPI; 97-55887/51.

N-PSDB; V17296.

Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis and therapy of cancer Example 11: Page 122-123; 208pp; English.

This sequence is the light chain variable region of the antibody of the invention. The antibody is an anti-CEA (carcinoembryonic antigen) antibody (806.077 Ab). Host cells or transgenic organisms transformed with DNA encoding the antibody, are used to make the antibody or administration. The conjugate is used in a medicament suitable for intravenous administration. The conjugate can be used for cancer therapy, selectively killing tumour cells. The antibody can be used for in vivo or in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUN-1998 (first entry)
Anti-CEA antibody 806.077 variable light chain.
Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy; cancer diagnosis; complementarity determining region; Fd chain.
Chimeric - Homo sapiens.
Chimeric - Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis and therapy of cancer claim 4; Page 138-139; 208pp; English.

This sequence is the light chain variable region of the antibody of the invention. The antibody is an anti-CEA (carcinoembryonic antigen) antibody (806.077 Ab). Host cells or transgenic organisms transformed with DNA encoding the antibody, are used to make the antibody or conjugate. The conjugate is used in a medicament suitable for intravenous administration. The conjugate can be used for cancer therapy, selectively killing tumour cells. The antibody can be used for in vivo or in vitro diagnosis of cancer.

Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                      29-APR-1997; G01165.
14-FEB-1997; GB-003103.
04-MAY-1996; GB-009405.
                                                                                                                            Sequence
                                                                                                                                              diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 14
W41397 standard; Protein; 107
W41397;
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Copley CG, Edge MD, Emery
WPI; 97-558987/51.
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                                                            y Match 100.0%;
Local Similarity 100.0%;
hes 11; Conservative
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29-APR-1997;
24
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MTQSPSSLSAS
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Similarity 100.0%;
11; Conservative
                                                                                                                                             of cancer.
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GB-009405.
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                                                                         Score 63; DB 29;
Pred. No. 3:52e+00;
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3.52e+00;
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RESULT ID W: AC W:

LT 15
W23953 standard; Protein; 107
W23953;

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PPT New humanised antibodies specific for glycated albumin - prepared by PT recombinant expression of humanised mouse antibodies, useful for, PT e.g. treating diabetic vasculopathy
Example 2; Page 15; 27pp; English.
The sequence is that of a humanised variable region of the A717 antibody light chain VL-1. The antibody has specificity for glycated albumin (GA) and is capable of neutralising the effects of GA in vivo. It can be used in the manufacture of therapeutics useful for the prophylactic treatment of complications of diabetes (especially diabetic vasculopathy and retinopathy) and atherosclerotic cardiovascular disease. The genetically engineered antibodies and may be easily prepared in pure form.
Sequence 107 AA;
                                                                    Matches
                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUN-1998 (first entry)
Chimeric humanised Mus musculus A717 antibody heavy chain.
Chimeric; humanised; human; murine; A717; antibody; heavy
variable region; diabetes; prophylactic treatment.
Chimeric - Mus musculus,
Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                           Cohen MP, Shearman CW; WPI; 98-076916/07. N-PSDB; V04637.
                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-1997; U11605.
27-JUN-1996; US-672176.
(EXOC-) EXOCELL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9749429-A1.
 24
                       4 mtqspsslsas 14
MTQSPSSLSAS
                                                                h 100.0%;
Similarity 100.0%;
11; Conservative
34
                                                              Score 63; DB 29; L
Pred. No. 3.52e+00;
0; Mismatches 0;
                                                                                                Length 107
                                                                Indels
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MPsrch_pp n on: protein - protein database search, using Smith-Waterman algorithm Tue Apr 20 14:03:38 1999; MasPar time 3.28 Seconds 125.736 Million cell updates/sec

Description: Perfect Score: Sequence: Title: >US-08-836-455-1_1 (24-34) from trans.pep (1 of 3) 63 1 MTQSPSSLSAS 11

fabular output not generated.

Scoring table:

PAM 150 Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir58 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 21.222; Variance 25.990; scale 0.817

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

	RESULT ENTRY TITLE ALTERNATE ORGANISM DATE	
y, A.; Katz, J.B.; Pillinger, M.; Ghosse Diamond, B. (1991) 174:1639-1652 racteristics of antibodies bearing an sociated idiotype. abel MAN immunoglobulin v region; immunoglobulin r; immunoglobulin v region; immunoglobulin r; immunoglobulin framework 2\ complementarity-determining 1\ framework 2\ complementarity-determining 2 checksum 237; Pred. No. 1.28e-03; Pred. No. 1.28e-03; pred. No. 1.28e-03; i Pred. No. 1.28e-03; O; Mismatches O; Indels O; Gamblementarity-determining 2 checksum 237	<pre>r 1</pre>	
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#title Molecular Characteristics of antibodies bearing
anti-DNA-associated idiotype.
#cross-references MUID:92078875
#accession PH0879
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##cross-references EMBL:M64856
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24 MTQSPSSLSAS 34
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Similarity 100.0%;
11; Conservative
Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, J. Exp. Med. (1992) 176:761-779

Both IgM and IgG anti-DNA antibodies are the process of the pr
                                                                                                                                                                                            PH1063 #type fragment
Ig 119ht chain V region (clone 202.33) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
15-Jun-1996
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heterotetramer; immunoglobulin
#length 62 #molecular-weight 6821 #checksum 8574
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Clonal characterization of the human IgG antibody repertoire
to Haemophilus influenzae type b polysaccharide. IV. The
less frequently expressed VL are heterogenous.
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Ig kappa chain V region (018) - human
#formal_name Homo sapiens #common_name man
13-Jan-1995 #sequence_revision 13-Jan-1995
09-May-1997
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                                                   ##molecule_type mRNA
##residues 1-103 ##label STA
##cross-references EMBL:x59187; NID:g52318; PID:e36167; PID:g1334064
##note the sequence of residues 1-8 and the corresponding
nucleic acid sequence are not shown
##molecule_type mRNA
##residues 1-103 ##label
                                  ##status
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##residues 1-97 ##label
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##experimental_source B cell, strain [NZB
FFICATION #superfamily immunoglobulin V r
Immunoglobulin
RDS #length 94 #checksum 1938
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$26332; $26331
$26309
                                                                                                                                                              Stark, S.E.; Caton, A.J.
J. Exp. Med. (1991) 174:613-624
Antibodies that are specific for a single amino acid interchange in a protein epitope use structurally
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Ig light chain V region - mouse (fragment)
Ig kappa chain V region
#formal_name Mus musculus #common_name house mouse
19-Mar-1998 #sequence_revision 19-Mar-1998 #text_c)
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#length 97 #checksum 1339
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Both IgM and IgG anti-DNA antibodies are clonally selective B cell stimulation i
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Ig 11ght chain V region (clone 202.54) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
15-Jun-1996
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Pred. No. 1.28e-03;
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##cross-references EMBL:X59185; NID:g52316; PID:e36165; PID:g1334063
[FICATION #superfamily immunoglobulin V region; immunoglobulin homo:

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**Tength 104 #molecular-weight 11443 #checksum 4741
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##cross-references EMBL:X75387
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J. Exp. Med. (1991) 174:613-624
Antibodies that are specific for a single amino acid interchange in a protein epitope use structurally of the structural of the struct
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anti-tetanus toxin 9F12 Fab light-chain - human (fragment)
#formal_name Homo sapiens #common_name man
13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
16-Feb-1997
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Ig kappa chain V region - mouse
#formal_name Mus musculus #common_name house mouse
13.Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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Pred. No. 1.28e-03;
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Mismatches 0;
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##cross references GB:J04577; NID:g623187; PID:g623189
IFICATION #superfamily immunoglobulin V region; immunoglobulin
NDS heterotetramer; immunoglobulin
#length 106 #checksum 2278
                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
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Similarity 100.0%;
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D.; Marshak-Rothstein, A.; Weigert, M.
J. Exp. Med. (1990) 171:265-297
Anti-Dula antibodies from autoimmune mice
                                                                                                                                                                                                                                                                                                                                                                                                                                      Shlomchik, M.; Mascelli, M.;
D.: Marshak-Rothstein, A.;
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Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C33936 #type fragment
Ig kappa Chain V region (VM113) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change
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#checksum 2162
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Pred. No. 1.28e-03
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FICATION #superfamily immunoglobulin v region; immunoglobulin
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Similarity 100.0%;
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Similarity 100.0%;
                    S36275
Ig lamb
                                                                                                                                                                                                                                                                                    S40366
                                                                                                                                                                                                                                                                                                       Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. (1993) 23:3248-3271
Expressed human immunoglobulin chi gen
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Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.
D.; Marshak-Rothstein, A.; Weigert, M.
J. Exp. Med. (1990) 171:265-297
Anti-DNA antibodies from autoimmune mice arise expansion and somatic mutation.
                                                                                                                                                                                            #length 107
                                                                                                                                                                                                      heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                     $40366 #type complete
Ig kappa chain V-J region - human
#formal_name Homo sapiens #common_name man
19-May-1994 #sequence_revision 26-May-1995
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                                                                                                                                         Conservative
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Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
     bb2/5  #type frågment;'
r lambda chain V region (clone alpha-FOG1-A4) -
(fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                  hypermutation.
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                                                                                                                                                                                                                                             1-107 ##label KLE
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#region complementarity-determining
#region framework 2\
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framework 3\
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Pred. No. 1.
0; Mismatc
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                                                                                                                                       Mismatches
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1.28e-03;
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$36256
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##cross-references EMBL:Z18842
IFICATION #superfamily immunoglobulin V region;
NOS heterotetramer; immunoglobulin
#length 107 #checksum 4341
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##cross-references EMBL:218827; NID:g33416; PID:g939909
##CRATION #superfamily immunoglobulin V region; immunoglobulin homology
**ROS**
**DS**
**Hength 107 #checksum 8985**
**Tength 107 #
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Similarity 100.0%;
11; Conservative
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Similarity 100.0%;
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Ig lambda chain '
   (fragment)
               #formal_name Homo sapiens #common_name man
03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. (1993) 12:725-734
Human anti-self antibodies with
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S36256
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[(fragment)
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Human anti-self antibodies with high specificity
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Pred. No. 1.28e-03;
0; Mismatches 0;
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#authors Griffiths, A.D.; Malmqvist, Marks, J.D.; Bye, J.M.;
Embleton, M.J.; McCafferty, J.; Baier, M.; Holliger, K.P.;
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
G.

# journal EMBO J. (1993) 12:725-734

# title Human anti-self antibodies with high specificity from phage
display libraries.

$ 536269

# # status preliminary; nucleic acid sequence not shown
# # molecule_type mRNA
# # residues 1-107 # label GRI
# # reross-references EMBL:Z18838; NID:g33422; PID:g939915

CLASSIFICATION # superfamily immunoglobulin v region; immunoglobulin
KEYWORDS Heterotetramer; immunoglobulin
SUMMARY # length 107 # checksum 6368

Query Match 100.0%; Score 63; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.28e-03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: Tue Apr 20 14:04:04 1999 Job time : 26 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

abular output not generated. n on: Tue Apr 20 14:02:18 1999; MasPar time 2.40 Seconds ----122.815 Million cell updates/sec

Title:
Description:
Perfect Score: >US-08-836-455-1_1 (24-34) from trans.pep (1 of 3) 63 1 MTQSPSSLSAS 11

Sequence:

Scoring table: PAM 150 Gap 11

Searched: 74019 segs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot35 1:swissprot

Statistics: Mean 21.723; Variance 21.843; scale 0.994

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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115	112	108	108	108	107	130	129	129	117	117	109	108	108	108	108	108	108	108	108	108	108	108	Length
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RESULT

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ALIGNMENTS

ОУ	Z W O	O O O O O O O O O O O O O O O O O O O	RESI ID AC DT
Db 4 MTQSPSSLSAS 14 Qy 24 MTQSPSSLSAS 34	Query Match 100.0%; Score 63; DB 1; Length 108; Best Local Similarity 100.0%; Pred. No. 4.67e-05; Matches 11; Conservative 0; Mismatches 0; Indels 0;	Ol-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE) IG KAPPA CHAIN V-I REGION (WAT). HOMO SAPIENS (HUMAN). EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA, EUTHERIA; PRIMATES. [1] SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS). MEDLINE; 95086080. HUANG DB., CHANG CH., AINSWORTH C., BRUENGER A.T., EULITZ SOLOMON A., STEVENS F.J., SCHIFFER M.; BIOCHEMISTRY 33:14848-14857(1994). [2] SEQUENCE OF 1-35. MEDLINE; 81267384. STEVENS F.J., WESTHOLM F.A., PANAGIOTOPOULOS N., SCHIFFER M., POPP R.A., SOLOMON A.; J. MOL. BIOL. 147:185-193(1981)[- THIS IS A BENCE-JONES PROTEIN. POPP R.A., SOLOMON A.; IMTUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; 3D-STRUCTURE. DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1. DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 2. DOMAIN 57 88 FRAMEWORK 2. DOMAIN 57 88 COMPLEMENTARITY-DETERMINING 3. DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3. DOMAIN 98 107 FRAMEWORK 4. DISULEID 23 88 107 FRAMEWORK 4. DISULEID 30 31 TN -> SD (IN REF. 2). NON_TER 108 108 SEQUENCE 108 AA; 11737 MW; 41A2388C CRC32;	SULT 1 KV1Y_HUMAN STANDARD; PRT; : p80362; 01-NOV-1995 (REL. 32, CREATED) 01-NOV-1995 (REL. 32, LAST SEQUENCE U
	0; Gaps 0;	PZ M.,	

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KV1P_HUMAN STANDARL,

P01608;

21-JUL-1986 (REL. 01, CREATED)

1 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDAT

1 01-JAN-1988 (REL. 05, LAST ANNOTATION UP

1 01-JAN-1988 (REL. 07, LAST ANNOTATION UP)
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Best Local
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EULITZ M., HILSCHMANN N.;
HOPPE-SEXLER'S Z. PHYSIOL. (
-!- THE C REGION OF THIS CHI
-!- THIS IS A BENCE-JONES P)
PIR; A01875; K1HUSW.
HSSP; P01607; 1IGM.
IMMUNOCLOBULIN V REGION; BE
                                                                                                                                                                                                        MEDLINE; 68362076.
HILSCHMANN N.;
HOPPE-SEYLER'S Z. P;
[2]
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    DISULFID
                                                                                                                   HILSCHMANN N., BARNIKOL H.U., HESS M., LANGER B., PONSTIN STEINMETZ-KAYNE M., SUTTER L., WATANABE S.; (IN) GAMMA GLOBULINS: STRUCTURE AND FUNKTION, FRANCK F., EDS., PP.57-74, ACADEMIC PRESS, NEW YORK, (1969).

1- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
                                                                                                                                                                                                                                         SEQUENCE.
                                                                                 DOMAIN
                                                                                                             PIR; A01874; K1HURY.
                                                                                                                                                           REVISIONS TO 39 AND 41.
HILSCHMANN N., BARNIKOL H.U., HESS M., LANGER B.,
SUTTER L., WATANABE S.;
                                                                                                                                                                                                                                                                         IG KAPPA CHAIN V-I REGION (RO)
HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JAN-1988 (REL. 06, LAST AUNOTATION UPDATE)
1G KAPPA CHAIN V-I REGION (SCW).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
EUTHERIA; PRIMATES.
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P01609;
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                                                      BENCE-JONES PROTEIN.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.
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FRAMEWORK 1.
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                 COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING
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         FRAMEWORK
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L-JAN-1988 (REL. 01, LAST SEQUENCE UPD)

IG KAPPA CHAIN V-I REGION (GAL).

EUGARYOTA; METAZOA; CHORDATA; VETAZOA;

[1]

SEQUENCE
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTRON MEDLINE; 76039968.

EPP O., LAITMAN E.E., SCHIFFER M., BIOCHEMISTRY 14:4943-4952(1975).

-1- THE C REGION OF THIS CHAIN HAS
                                                        MEDLINE;
PALM W.,
                                                                                         KVIO_HUMAN STANDARD; PRT; 108 AA. PD1607; P1607; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01 MAR-1992 (REL. 21, LAST ANNOTATION UPDATE) 1G KAPPA CHAIN V-I REGION (REI). HOMO SAPIENS (HUMAN). EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
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                                                HOPPE-SEYLER'S Z. PHYSIOL.
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TURN
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SCIENCE 169:56-59(1970).
SCIENCE 169:56-59(1970).
-!- THE C REGION OF THIS CHAIN HA
-!- THIS CHAIN WAS ISOLATED FROM
PIR; A01872; KIHUOU.
HSSP; P01607; 2FGW.
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MEDLINE; 70201507
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EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
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                                                                                                                                                              IMMUNOGLOBULIN
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4 MTQSPSSLSAS 34
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Pred. No. 4.67e-05;
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                              COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.

COMPLEMENTARITY-DETERMINING
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COMPLEMENTARITY-DETERMINING
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FRAMEWORK 1.
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4B089785 CRC32;
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A WALDENSTROM'S MACROGLOBULIN
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                                               SEQUENCE.

MEDLINE; 72053133.

MILSTEIN C.P., DEVERSON E.V.;
BIOCHEM. J. 123:945-958(1971).

-:- THE C REGION OF THIS CHAIN H.
PIR; A01865; K1HUDE.
HSSP; F01607; 1FVC.
IMMUNGLOBULIN V REGION.
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21-JUL-1986 (REL. 01
01-JAN-1988 (REL. 06
IG KAPPA CHAIN V-I R
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DOMAIN
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EUKARYOTA; MI
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SEQUENCE: 83273707.
MEDLINE: 83273707.
GONI F., FRANGIONE B.;
PROC. NATL. ACAD. SCI. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                EUTHERIA;
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THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST
3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.
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Similarity 100.0%;
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Similarity 90.9%;
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Pred. No. 4.67e-05;
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FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.
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COMPLEMENTARITY-DETERMINING
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No. 4.67e-05;
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21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDA
01-JAN-1988 (REL. 05, LAST ANNOTATION UF
IG KAPPA CHAIN V-I REGION (HAU).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRAT?
MEDLINE; 71032830.
WATANABE S., HILSCHMANN N.;
HOPPE-SEYLER'S Z. PHYSIOL, CHEM.
                                            SEQUENCE.
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-!- THIS IS A BENCE-JONES PROTEIN.
PIR; A01861; KIHUAG.
HSSP; P01607; IREI.
IMMUNOGLOBULIN V REGION; BENCE-JON
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DOMAIN
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J. BIOL. CHEM. 244:3550-3560(1969).
-!- THE C REGION OF THIS CHAIN HAS
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EUTHERIA; PRIMATES.
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HOMO SAPIENS (HUMAN).
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21-JUL-1986 (REL.
01-JAN-1988 (REL.
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, LAST SEQUENCE UPI
, LAST ANNOTATION (
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FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.
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Pred. No.
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COMPLEMENTARITY - DETERMINING FRAMEWORK 4.

BY SIMILARITY.
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1. No. 4.67e-05;
Mismatches C
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AS THE INV (3) MARKE
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Mismatches 0;
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         (3) MARKER
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-!- THE STRUCTURE OF THE V REGION WAS DE REPLACEMENT METHODS USING THE KNOWN
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P01594;
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HSSP; P01607; 1IGM.
IMMUNOGLOBULIN V REGION;
                                                                                                                                                                                                                                                                                                THE KAPPA CHAIN REI.

-I- THE C REGION OF THIS CHAIN HAS
-I- THIS IS A BENCE-JONES PROTEIN.
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SEQUENCE
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SCHIECHL H., HILSO
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-I REGION (AU).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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HOPPE-SEYLER'S Z. PHYSIC
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DOMAIN
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DOMAIN
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PIR; A01868; K
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MTQSPSSLSAS 14
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COMPLEMENTARITY-DETERMINING
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COMPLEMENTARITY - DETERMINING
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
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                                                                                          B455AF00 CRC32;
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                     DB 1; Lens
4.67e-05;
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H.J.;
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4.67e-05;
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Best Local
   Query Match
Best Local Similarity
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EULITZ M., LINKE R.P.;
HOPPE-SEYLER'S Z. PHYSIOL. CH
-!- ANOTHER FORM THAT LACKED
-!- THIS CHAIN WAS ISOLATED F
PIR; A01879; K1HUMV.
HSSP; P01607; 2FGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KV5H_MOUSE STAI
P01641;
21-JUL-1986 (REL. (
21-JUL-1986 (REL. (
01-OCT-1996 (REL.
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KV1T_HUMAN STAN

P01612;
21-JUL-1986 (REL. (
21-JUL-1986 (REL. (
21-JUL-1988 (REL. (
01-JAN-1988 (REL. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMUNOGLOBULIN V REGION.

DOMAIN 1 23

DOMAIN 24 34

DOMAIN 35 49

DOMAIN 50 56

DOMAIN 57 88

DOMAIN 89 98

DOMAIN 99 108
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DISULFID
NON_TER
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DOMAIN
DOMAIN
                                                                              DISULFID NON_TER
                                                                                                                                                                                                                                                                                                                        MAX E.E., SEIDMAN J.G., CELL 21:793-799(1980). EMBL; K00880; G197444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 173B).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                     MMUNOGLOBULIN
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                                                                                                                                                                                                                                                                                   21:
, K00880; G1.
1924; KVMS3B.
                                                                                                                                                                                                                                                                                                          AO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity 100.0%;
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81064681.
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34, LAST ANNOTATION
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                                                                                                                                                                                                                                                                     SIGNAL
                                                          MW;
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ED RESIDUES 1-3 WAS ALSO FOUND.
D FROM A MYELOMA PROTEIN.
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Score 63; DB 1; I
Pred. No. 4,67e-05;
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.
                                                                                             FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING
BY SIMILARITY.
                                                                                                                                                    COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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                                                          38F2B08C CRC32;
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                       Length 117;
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BENTIEY D.L., RABBITTS T.H.;

CELL 32:181-189(1983).

EMBL; 700244; 6185970; -.

EMBL; K01322; G185994; -.

EMBL; K01324; G185998; -.

EMBL; W00558; G33177; -.

R PIR; A01881; K1HU11.

R PIR; A01881; K1HU11.

R PIR; A01056; A21056.

R PIR; A21056; A21056.

R SP; P01607; IDEB.

HSSP; P01607; IDEB.
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Best Local
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13-AUG-1987 (REL. 05, LAST
01-NOV-1990 (REL. 16, LAST
IG KAPPA CHAIN PRECURSOR V
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P01601;
21-JUL-1986 (
21-JUL-1986 (
01-MAY-1991 (
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NON_TER
SEQUENCE
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CHAIN
DOMAIN
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EUTHERIA; PRIMATES.
SEQUENCE FROM N.A.

MEDLINE; 85014148.

KLOBECK H.G., COMBRIATO G., ZACHAU H.G.;

NUCLEIC ACIDS RES. 12:6995-7006(1984).

EMBL; K02134; G185822; -.

EMBL; X00966; G296685; ALT_TERM.
                                                                                                                                    HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 81098966.
BENTLEY D.L., RABBITTS T.
NATURE 288:730-733(1980).
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                                                                                                                                                                                                                                                                                                KV1X_HUMAN
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EDLINE; 81098966.
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                                                                                                                                                                                                                                                                                                                                                                            24 MTQSPSSLSAS 34
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Pred. No. 4.67e-05
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DR PIR: A01884; K1HUDI.

DR HSSP; PO1607; 1FGV.

KW IMMUNOGLOBULIN V REGION; SIGNAL.

FT SIGNAL 1 22

FT SIGNAL 1 23

FT CHAIN 23 129

FT DOMAIN 23 129

FT DOMAIN 57 71

FT DOMAIN 72 10

FT DOMAIN 79 110

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MPsrch_pp n on: protein - protein database search, using Smith-Waterman algorithm Tue Apr 20 14:02:43 1999; MasPar time 4.27 Seconds 128.383 Million cell updates/sec

Description: Perfect Score: Sequence: >US-08-836-455-1_1 (24-34) from trans.pep (1 of 3) 63 1 MTQSPSSLSAS 11

abular output not generated.

Scoring table: PAM 150 Gap 11

Searched: 165420 segs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb16

1:sp_archea 2:sp_bacter1a 3:sp_fung1 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 20.775; Variance 22.138; scale 0.938

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES.

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ORF40.	PUTATIVE UREASE OPERON	T21H3.5 PROTEIN.	ANTIGEN, B-CELL RECEPT	NUCLEAR PROTEIN SA-1.	TYROSINE KINASE CEK6 R	BM28 HOMOLOGUE.	NUCLEAR FACTOR, ERYTHR	ACETOLACTATE SYNTHASE	PUTATIVE TRANSCRIPTION	С06В3.9.	MONOCLONAL ANTIBODY KA	HRV FAB N27-VL (FRAGME	KAPPA (FRAGMENT).	TYPE II COLLAGEN ANTI-	HRPJ3.	IG KAPPA CHAIN (FRAGME	IG KAPPA CHAIN (FRAGME	IG KAPPA CHAIN PRECURS	ACI	HYPOTHETICAL 47.7 KD P	D1025.1.	ANTI-HIV-1 GP120 V3 LO	V KAPPA (FRAGMENT).	NEVALUE (FINAGMENT).
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ALIGNMENTS

RROCOCETTI	Qy RESULT	Ma Be	SORRARRA	# # 000 E	SU
01-MAY-1997 (TREMBLREL. 03, CREATED) 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE) 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE) 01-HOG-1998 (TREMBLET). (FRAGMENT). HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES. [1] SEQUENCE FROM N.A.	7 MTQSPSSISAS 17 24 MTQSPSSISAS 34 27 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Query Match 100.0%; Score 63; DB 4; Length 50; Best Local Similarity 100.0%; Pred. No. 1.08e-04; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	KLOBECK H.G.; SUBMITTED (AUG-1987) TO EMBL/GENBANK/DDBJ DATA BANKS. [2] SEQUENCE OF 36-50 FROM N.A. MEDLINE; 87259967. KLOBECK H.G., COMBRIATO G., ZACHAU H.G.; NUCLEIC ACIDS RES. 15:4877-4888(1987). EMBL; X05929; E12675; EMBL; X05929; E12675; SEQUENCE 50 AA; 5486 MW; 65586C19 CRC32;	IN THE CELL LINE JI (CLONE JIP). HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES. [1] SEQUENCE FROM N.A.	15533; 15533; 1-NOV-1996 (TREMBLREL 01. 1-NOV-1996 (TREMBLREL 01. 1-NOV-1996 (TREMBLREL 01. 1-NOV-1996 (TREMBLREL 01. 1-NOV-1996 (TREMBLREL 01.)

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SUBMITTED (SEP-1996) TO
EMBL; Y08148; E274854; -
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EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
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01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
VASOACTIVE INTESTINAL POLYPEPTIDE HYDROLYZING AUTOA
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01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
VASOACTIVE INTESTINAL POLYPEPTIDE HYDROLYZING AUTOANTIBODY LIGHT CHAIN
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
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                                   Score 63; DB 4; I
Pred. No. 1.08e-04;
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0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA; TETRAPODA;
                                                                                                                                                               3D1FEE15 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C1E164AA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249B7EC3 CRC32;
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d. No. 1.08e-04;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No. 1.08e-04; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYDROLYZING AUTOANTIBODY LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
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                                                                                            Length 107
                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B.M.;
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Best Local S
Matches 1
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Best Local S
Matches 1
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SEQUENCE
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JUUL L., HOUGS L., BARINGTON T.;
SUBMITTED (SEP-1997) TO EMBL/GER
EMBL; Y14865; E1169998; -.
PFAM; PF00047; 19.
NON_TER 117
SEQUENCE 117 AA; 12748 MW; (
                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-BLOOD;
                                            26 MTQSPSSLSAS
||||||||||
24 MTQSPSSLSAS
                                                                                                                                                                                                                                             HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                  MTQSPSSLSAS
                                                                                       h 100.0%;
Similarity 100.0%;
11; Conservative
                                                                                                                                                                                                                                       PRIMATES
                                                                  36
                                              34
                                                                                                                                                                                                                                                                                                                                                                                     34
                                                                                                                                                                                                                                                                             05, CREATED)
05, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
REGION, KAPPA LIGHT CHAIN (FRAGMENT).
                                                                                                                                                                              EMBL/GENBANK/DDBJ
                                                                                                 Score 63; DB 4; I
Pred. No. 1.08e-04;
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                                                                                       0
 PRT;
                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                             034081EF CRC32;
                                                                                       Mismatches
113
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                                                                                                                                                                              DATA
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                                                                                                           Length 117;
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                                                                                      Indels
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                                                                                     Gaps
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RESULT 7
ID Q15982
AC Q15982;
DT 01-NOV-1996 (TREMBLREL. 01, C:
DT 01-NOV-1996 (TREMBLREL. 01, L:
DT 01-JUN-1998 (TREMBLREL. 06, L:
DE RHEUMATOLD FACTOR C6 LIGHT CH:
GN V<KAPPA>1.
                                                                                                                                                                                                                                                                                                                                                                                                                    O14535 PRELIMINARY; P
O14535; PREMBLREL 05, CRE
O1-JAN-1998 (TREMBLREL 05, LAS:
O1-JAN-1998 (TREMBLREL 07, LAS:
O1-AUG-1998 (TREMBLREL 07, LAS:
HV FAB N6-VL (FRAGMENT).
HOMO SAPIENS (HUMAN).
EUCHERIA; METAJOA; CHORDATA; VI
                                                                                                                                                                                                                                                                                                            ITOH K., SUZUKI T.;
SUBMITTED (AUG-1997) TO EI
EMBL; AB006842; D1023041;
FFAM; PF00047; 19.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                      6 MTQSPSSLAAS 16
||||||||||
24 MTQSPSSLSAS 34
                                                                                                                                                                                                                 Similarity 90.9% 10; Conservative
                                                                                                                                                                                                                                                                               113 AA;
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113
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; 12207
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           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
CHAIN (FRAGMENT).
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                               Score 61; DB 4; L
Pred. No. 3.94e-04;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA; TETRAPODA;
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                                                                                         116
                                                                                         B
                                                                                                                                                                                                                                            Length 113;
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RESULT
ACCORDANCE
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Best Local S
Matches 1
Query Match
Best Local Similarity
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Best Local
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HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA; CHORDATA; VIEUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                       000289;
000289;
01-JUL-1997;
01-JUL-1997;
01-AUG-1998;
                                                                        PFAM; PE
                                                                                                   SEQUENCE FROM N.A.

KONTERMANN R.E., WING M.G., WINTER G.);

NAT. BIOTECHNOL. 15.629-631(1997).

EMBL, Y13056; E315281; -.

PEAM; PF00047; 19.

NON TEP
NON TEP
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ERMEL R.W., KENNY T.P., CHEN P.P., ROBBINS
ARTHRITIS REUM. (MUNCH.) 36:380-388(1993).

EMBL; S56182; G298561; -.

PFAM; PF00047; 1g.

NON_TER 1 1

NON_TER 1 16
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EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GODDARD A., YUAN J., ZHU ;
SUBMITTED (FEB-1998) TO EI
EMBL; AF048775; G2911502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                     SINGLE-CHAIN
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                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 MTQSPSTLSAS
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10; Conser
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116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239
239 AA;
                                                          240
                                                                                                                                                                                                                                                                                                     (TREMBLREL. 04, CREATED)
(TREMBLREL. 04, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDAT
N FV FRAGMENT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.8%;
larity 90.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.8%;
larity 90.9%;
Conservative
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116
12528 Þ
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25262 MW;
                                                        240
25569
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 96.8%;
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EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                        WW;
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Pred. No.
1; Misma
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
 Score
Pred.
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Pred. No. 3.94e-04
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                                                                                                                                                                                                                                             VERTEBRATA;
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                                            6472A9C9 CRC32;
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 No 1;
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 DB 4; L
3.94e-04;
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3.94e-04;
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                                                                                                                                                                                                                                             TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATA BANKS
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Matches 1
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Best Local Similarity
Matches 10; Conser
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                   ULT 12
014540; PRELIMINARY;
014540; (TREMBLREL 05,
01-JAN-1998 (TREMBLREL 05,
01-JUG-1998 (TREMBLREL 07,
01-AUG-1998 (TREMBLREL 07,
HRV FAB 027-VL (FRAGMENT).
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01-JUL-1997 (
01-AUG-1998 (
SINGLE-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y1
PFAM; PF
NON_TER
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 11
043689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

GODDARD A., YUAN J., ZHU Z., CARTER P.;
SUBMITIED (FEB-198) TO EMBL/GENBANK/DDBJ

EMBL; AF048774; G2911500; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KONTERMANN R.E., WING M.G., WINTER NAT. BIOTECHNOL. 15:629-631(1997). EMBL; Y13057; E315275; -.
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EUKARYOTA; METAZOA; C
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
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HOMO SAPIENS (HUMAN).
CHORDATA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       043689;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                            24 MTQSPSSLSAS
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                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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244 AA;
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244 AA;
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7 (TREMBLREL. 0
8 (TREMBLREL. 0
IN FV FRAGMENT
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larity 90.9%;
Conservative
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llarity 90.9%;
Conservative
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26025
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04, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDAT
(FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                   Score 61; DB 4; pred. No. 3.94e-04
1; Mismatches
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LAST SEQUENCE UPDATE)
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                                                      CREATED)
LAST SEQUENCE UI
LAST ANNOTATION
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Pred. No. 3.94e-04
1; Mismatches (
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SAPIENS

(HUMAN)

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Best Local S
Matches 1
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Best Local S
Matches 1
            NON_TER
                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                         LT 14
099818
099818;
01-MAY 1997 (TREMBLREL. 03, CREATED)
01-MAY 1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
ANTI-SZDNA ANTIBODY LIGHT CHAIN VARIABLE REGION (FRAGMENT).
    SEQUENCE
                             SUBMITTED (DEC-1996) TO EMBL; U82258; G1773057; PFAN; PF00047; ig.
                                                             SEQUENCE FROM N.A. SUENAGA R.;
                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                         EMBL;
PFAM;
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KIM I.J., CHOI I.H., CHUNG H.K.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; U88067; G1850548; -
                                                                                                                                                                                                                                                                                                                                                                           CHING J.H., LEE S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).
MUS CULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                           SEQUENCE
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P97771
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EUTHERIA; P
[1]
                                                                                                                                                                                                                                       137 LTQSPSSLSAS 147
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SEQUENCE 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITOH K., SUZUKI T.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AB006849; DIO23047; -.
PEAM; PF00047; 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-PBL;
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Local Similarity 90.9%;
hes 10; Conservative
                                                                                                                                                                                                                             24
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PF00047; ig.
                                                                                                                                                                                                                                                                1 Similarity
10; Conserv
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241
241 AA;
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              108
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larity 90.9%;
Conservative
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113 113
AA; 12383 MW;
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26086
 11792 MW;
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                                           EMBL/GENBANK/DDBJ DATA BANKS
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                                                                                                                                                                                                                                                                           Score 56; DB 11;
Pred. No. 9.20e-03;
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Pred.
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876D5BA3 CRC32;
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                                                                                                                                                                                                                                                                 Mismatches
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No. 7.47e-04;
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Query Match

87.3%;

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Matches
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Matches
  time
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P97408;
P97408;
01-MAY-1997
01-MAY-1997
01-JUN-1998
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MEDLINE; 97257994.
ITO H.O., UEDA T., HASHIMOTO Y., IMO;
CELL. MOL. LIFE SCI. 53:51-60(1997).
EMBL; U69539; G1731667; -.
PFRM; PF00047; 19.
NON TEE
                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FRAGMENT).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE II COLLAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
completed: Tue Apr
ne : 37 secs.
                                                                                                                                                                                                              Y Match 85.7%;
Local Similarity 81.8%;
les 9; Conservative
                                                                                                          24
                                                                                                                                                         4 LTQSPTSLSAS 14
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8; Conservative
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(TREMBLREL. 03, LAST SEQUENCE UPDATE)
(TREMBLREL. 06, LAST ANNOTATION UPDATE)
LAGEN ANTIBODY KAPPA LIGHT CHAIN VARIABLE
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11093 MW;
                      20 14:03:20 1999
                                                                                                                                                                                                            Score 54;
Pred. No.
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de lyase.	e E	uence of pro	Of	the S	/FIPV chimeric s	FECV/FIPV chimeric sp	Feline enteric corona	E2 protein of Canine	Ň	CCVInsavc spike prote	Rat OCT-1 protein.	Mouse CRTAM.	aromyce	ons	Light chain variable	o	secret	Hepatitis GB virus (H	beta.	Human CD22 antigen.	hocyte-sp	occus	ocystis d	rial delta-6-de	Hepatitis GB virus (H	Native CD26.
(A	45	4.5	.45e+0	45	.45e+0	.45e+0	.45e+0	4.5	.45e+0	.4.	.45e+0	.45e+0	.45e+0	.45e+0		.45e+0		7.02e+02	٠	7.02e+02	٠	.02e+0	7.02e+02	.02e+0		5.83e+02

ALIGNMENTS

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W09722699-A2.
26-JUN-1997.
19-DEC-1996; U20757.
13-DEC-1996; US-575762.
20-DEC-1995; US-575762.
26-JAN-1996; US-591965.
                                                                                                                                                                                   Region
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W27119 standard; Protein; 145 AA.
W27119;
04-JAN-1998 (first entry)
Murine monoclonal anti-idiotype antibody 11D10 VL region.
Monoclonal antibody 11D10; anti-idiotype antibody; mucin;
human milk fat globule; HMFG; tumour; breast cancer; vaccine.
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Key
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(KENT ) UNIV KENTUCKY.
Chatterjee M, Chatterjee SK,
                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                 /label= CDR1
/note= "complementarity determining region
55..69
                                                                        /label= CDR3
/note= "complementarity determining region 118..127
/label= FR1
/note= "framework region 4"
                                                                                                                                                                                                                                                                                              /label= Sig_peptide
21..145
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                                                                                                                          /label= FR3
/note= "framework region
109..117
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/note= "framework region 1"
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'note- "complementarity determining region 2"
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'note= "framework region 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PT against human milk fat globule disease associated tumours,
PT especially breast cancer
PS Claim 9; Page 94; 130pp; English.
CC This polypeptide sequence comprises the light chain variable region
CC (VL) of monocional anti-idiotype antibody 11D10 produced by
CC hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
CC naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype
CC response. It elicits an immune response against a specific epitope
CC of a high mol.wt. mucin of human milk fat globule (HMFG). It
CC induces an immunological response to HMFG in mice, rabbits, monkeys
CC and patients with advanced HMFG-associated tumours. Pharmaceutical
CC compositions and vaccines comprising 1D10, 1D10 polypucptides
CC and/or 11D10 polynucleotides (see also T85149-50) are claimed.
CC Also claimed are diagnostic kits and methods of using 1D10, 1D10
CC polypeptides and/or 1D10 molypucleotides, including methods of
CC treating HMFG-associated tumours. 1D10 is also used in a claimed
detect or quantify anti-HMFG antibody.
                                                                   Matches
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12-AUG-1994; U09293.
12-AUG-1993; US-10649
(UTEM) UNIV TEMPLE.
Glordano A;
                                                                                                                                  DNA encoding retinoblastoma suppressor.protein, pRB2 - and recombinant cell lines, for the diagnosis and suppression of cells infected with adenovirus ElA. Claim 10: Page 19-22: 29pp; English.

The retinoblastoma tumour suppressor protein, pRb2, binds to the ElA transforming domain, and is useful in the diagnosis of cells infected with adeno virus ElA or a related virus. The protein may be administered as a cell growth suppressor to infected cells e.g. retinoblastoma interocular cancer cells, and may be useful for identifying other DNA tumour virus oncoproteins. Sequence 1082 AA;
                                                                                                                                                                                                                                                                                                                                 WPI; 95-098768/13.
N-PSDB; Q82748.
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pRb2 retinoblastoma tumour suppressor protein.
Retinoblastoma; tumour suppressor; pRb2; diagr
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R65017 standard; Protein; 1082 AA
R65017;
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US-106493.
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                                                           Score 50; DB 13; Le
Pred. No. 2.73e+02;
1; Mismatches 1;
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Pred.
0; M
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Chis is the specifically claimed N-terminal amino acid sequence of the control of the nicroorganisms, or their enzymatic extracts, able invention relates to microorganisms, or their enzymatic extracts, able introgen) source. The invention also relates to new N-acetylamino-alcohol hydrolases (NAHH) from the microorganisms for preparation of chiral 1-amino-4-hydroxymethyl-2-cyclopentene from N-acyl precursors. Compared with other methods, this method of preparation involves fewer stages and does not require lithium aluminium hydride or other expensive
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Best Local
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01-JAN-1986; AU-042347.
(ELIL) ELI Lilly and Co.
Ingolia TD, Queener SH, S:
WPI; 90-124016/17.
                                                                                                                                                                           N-PSDB; Q04071.

Iso-penicillin N synthetase activating sequences isolated from DNA from Cephalosporin acremonium and used to increase antibiotic prodn. Disclosure; pp; English.

This enzyme can be used to produce isopenicillin N from the tripeptid delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine. Isopenicillin N is starting material for penicillin N and other cephalosporins. The greapotential use of the enzyme is to condense other tripeptides into now
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence encoding Isopenicillin N synthetase activity Iso-penicillin N synthetase; Cephalosporin acremonium; antibiotic. Cephalosporin acremonium. AU8942347-A.
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R04101;
10-SEP-1990 (first entry)
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30-MAY-1997; E02838.
18-APR-1997; CH-000908.
30-MAY-1996; CH-001359.
10-FEB-1997; CH-000282.
                                                                                                                                                   See also
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Brux F, Burgdon
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WPI; 98-032639/03.
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W09745529-A1.
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Local Similarity 100.08;
Local Similarity 100.08;
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Q04022
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Burgdorf K, Duc
                                                                                                                 338 AA;
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Etter K, Guggisberg
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Pred. No. 4.00e+02;
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re 48; DB 1; Le
1. No. 4.00e+02;
Mismatches 1;
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08-AUG-1986; 895008.

08-AUG-1986; US-895008.

08-AUG-1986; US-895008.

(ELIL) ELI LILLY & CO.

Ingolia TD, Queener SW, S

WPI; 90-044769/06.
                                                                                                                                                                                                                                            21-APR-1985; U5-72587.
22-APR-1985; US-72587.
18-NOV-1985; US-799384.
08-AUG-1986; US-895008.
(ELIL ) ELI LILLY & CO.
Ingolia TD, Queener SW, SWPI: 86-325839/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant DNA compounds encoding isopenicillin-N-synthetase used to produce vectors for improving fermentation efficiency and yield of penicillin antibiotic-producing organisms, etc. Claim 4; page 25; 40pp; English.

The protein is encoded in plasmid pPS19 and plasmid pS24. It has been used to construct novel E. coli expression vectors that drive expression of a stable, active, and novel isopenicillin-N-synthetase in E. coli. See also Q03267.
                                                                                                        N-PSDB; N60414.

New DNA encoding iso-penicillin N synthetase - for use in vectors permitting high level expression, esp. in prodn. of penicillin and cephalosporin antibacterials claim 28; page 86.7; 113pp; English.

Isopenicillin N synthetase (IPS) can be expressed using a vector which permits high level expression of TPS activity in E.coli. The IPS from E.coli forms isopenicillin N from delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine, and is also useful for condensing other tripeptides to form new antibiotics.
                                                                                                                                                                                                                                                                                                                                                           Cephalosporin acremonium AU8656431-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R03733 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                              P60508
                                                                                                                                                                                                                                                                                                                                                                                                                                       P60508 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                             30-OCT-1986.
                                                                                                                                                                                                                                                                                                                                                                                    Isopenicillin N synthetase Isopenicillin N synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isopenicillin-N-synthetase sequence 338 AA;
50 gvdlpwl 56
                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 GINLHWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 gvdlpwl
                                       4.
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                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                         Conservative
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                                                                                              A
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                                                      77.48;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.48;
57.18;
                                                                                                                                                                                                                                                             Samson
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                                                                                                                                                                                                                                                                                                                                                                                                                                           339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338
                                      Score 48; DI
Pred. No. 4.(
2; Mismatc)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 2; I
Pred. No. 4.00e+02;
2; Mismatches 1
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                                                                Length 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probetecting exposure to radiation or radio-mimetic agents - by correlation with a protein, such as transferrin receptor, present on the surface of red blood cells of a mammal psychology page 61-62; 83pp; English.

This polypeptide comprises the rat transferrin receptor (TR). Claimed methods for detecting a mammal spior exposure to radiation or radiomimetic agents (RAs) involve: isolating red blood cells from the mammal, and detecting the quantity of TRs on the red blood cells from the mammal, and detecting the quantity of TRs on the red blood cells is correlated with the mammal's prior exposure. It is possible to assess accurately cannotity of TRs on the red blood cells is correlated with the mammal's prior exposure and to directly study the effects of complative lifetime exposure and to directly study the effects of clow doses of radiation, e.g. on cancer risk and other delayed responses. The limited amount of blood necessary permits the test to be conducted as frequently as desired. The test's sensitivity, and the lethal dose ranges.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conse
Detecting exposure to radiation or radio-mimetic agents - by correlation with a protein, such as transferrin receptor, presenthe surface of red blood cells of a mammal Disclosure; Page 63-65; 83pp; English.

This polypeptide comprises the human transferrin receptor (TR). Claimed methods for detecting a mammal's prior exposure to radiation or radiomimetic agents (RAs) involve: isolating red blood cells from the mammal, and detecting the quantity of TRs on the blood cells using e.g. an antibody raised against the TR. The quantity of TRs on the red blood cells using e.g. an antibody raised against the TR. The quantity of TRs on the red blood cells using e.g. an antibody raised against the the grantity of TRs on the red blood cells using e.g. an antibody raised against the TR. The quantity of TRs on the red blood cells using e.g. an antibody raised against the TR. The quantity of TRs on the red blood cells using e.g. an antibody raised against the TR. The quantity of TRs on the red blood cells using e.g. and the the TR. The quantity of TRs on the red blood cells using e.g. and the transfer of the TR. The quantity of TRs on the red blood cells using e.g. and the transfer of TRs on the grantity of TRs on 
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21-0CT-1995; US-547197.
24-0CT-1995; US-547197.
(UYNY) UNIV NEW YORK STATE RES FOUND.
Glomski CA, Gong JK;
WPI; 97-259141/23.
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21-OCT-1996; US-547197.
24-OCT-1995; US-547197.
(UYNY) UNIV NEW YORK STATE RES FOUND
Glomski CA, Gong JK;
WPI; 97-259141/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-1997 (first entry)
Human transferrin receptor.
Radiation; radiomimetic; exposure; transferrin receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Radiation; radiomimetic;
red blood cell; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens. WO9715830-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              red blood cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 8
W22213 standard; Protein; 760
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57.18;
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Pred. No. 4.00e+02;
3; Mismatches 0;
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                Query Match
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Best Local S
Matches
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Best Local
                                                                                                                           D-amino acid oxidase, prodn. -
by culture of E.coli transformants contg. expression vectors
originated from Fusarium solani M-0718.
Disclosure: Fig 9; 38pp; English.
E.coli transformed to express DAO, which catalyses the enzymatic
conversion of cephalosporin C to 7-beta-(5-carboxy-5-
oxopentanamido)cephalosporanic acid (keto-7ACA). 7ACA is an
important starting point for the production of cephem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R04066 stand
R04066;
R04066;
03-SEP-1990
                                                                                                          antibiotics.
356
                                                                                                                                                                                                                                                                                                                                              (FUJI) Fufisawa Pharm KK. Isogai T, Ono H, Kojo H; WPI; 90-117771/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T.variabilis D-amino acid oxidase gene product. D-amino acid oxidase; cephalosporin; cephem; E. Trigonopsis variabilis. EP-364275-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mechanisms such as immune response etc.

Disclosure; p; Japanese.

This polypeptide is involved in protective mechanisms such as response, cell growth and activation of protective functions. sequence 321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-1990.
12-OCT-1989; 310483.
13-OCT-1988; JP-260332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              low doses of radiation, e.g. on cancer-risk and other delayed responses. The limited amount of blood necessary permits the test to be conducted as frequently as desired. The test's sensitivity, extending from 0.1 cGy to over 600 cGy, spans both the environmental and the lethal dose ranges.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide and DNA encoding it - related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DAIN) Dainippon Pharm KK. WPI; 88-068419/10.
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P81342 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JUL-1986; 167518.
16-JUL-1986; JP-167518.
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                                         Similarity
                   4;
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larity 57.18;
Conservative
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57.1%;
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57.18;
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            Score
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2; M
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Pred. No. 5.83e+02;
2; Mismatches 1
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4.00e+02;
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RESULT
ACC RA4
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TO THE SOLUTION OF THE 
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Polypeptide Tragments of CD26 - are capable of disrupting binding of CD45 and CD26 and thus interfering with T-cell activation SEXample; Pages 46-48; 73pp; ED31sh.

CC26 is a human T cell antivation antigen originally identified by its reactivity with the MAb Tal. C26 CDNA library was constructed from human PHA-activated T cells using the CDM7 vector.

Fragments of CD26 can be preped in the following manner.

CD26 Xbal-Sphi cDNA fragment is ligated to the vector RCSR-alpha-26 Xbal-Hindli DNA fragment and the linker Q46092.

The linker introduces an in-frame stop codon that results in the deletion of the segment of CD26 from AA 594 to the carboxy terminus of the wild-type protein. This deletion mutant, shown carboxy terminus given in R40917.

Sequence 593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
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Best Local Similarity
Matches 4; Consei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.

W09316102-A.

19-AUG-1993.

09-APR-1992;

06-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R40916 standa
R40916;
05-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DAND) DANA FARBER CANCER INST INC
Morimoto C, Schlossman SF, Tanaka
WPI; 93-272827/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA fragment encoding D-amino acid oxidase - which is a useful enzyme for the catalytic oxidative deamination of D-amino acids. Claim 1; page 583-4; 12pp; japanese.
D-amino acid oxidase catalyses the oxidative deamination of D-amino acids. It is used in the sepn. of L-amino acids from racemates, in the prepn. of ketoic acid from D-amino acid, in amino acid analysis, etc. The enzyme can oxidise cephalosporin C to 7-beta-(5-carboxy-5-oxopentanamide)cephalosporanic acid, which reacts with hydrogen peroxide to give 7-beta-(4-carboxybutanamide)-cephalosporanic acid. These cpds. are important intermediates for synthesis of cephalosporin type antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of a CD26 fragment lacking a portion of the carboxy terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ASAH ) ASAHI CHEMICAL WPI; 87-359677/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D-amino acid oxidase.
D-amino acid oxidase;
oxidative deamination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149
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12-MAY-1986; JP-106663.
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P70388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activation antigen; monoclonal antibody Tal; CD26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-832211.
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57.1%;
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Pred. No. 5.83e+02;
2; Mismatches
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Best Local Similarity
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28-APR-1993; U07923.
19-AUG-1993; US-934162.
21-AUG-1992; US-934162.
(DAND ) DANA FARBER CANCER I:
CONTROL C Schlossman S,
                                                                                                                                                                                                                                                                                                                                                                                        uery Match
                                                                                                                                                                                                       W43411 standard; W43411;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 56-58; 85pp; English.

The sequences given in R54612-14 represents analogues of the human T cell activation antigen CD26 which have internal deletions. The analogues pref. lack residues 3-9 or 24-34. These analogues are soluble under physiological conditions and lack enough amino acid residues to render them susceptible to cleavage by signal peptidase. The peptide fragments and analogues are useful as immune or responsestimulating therapeutics, eg. they may be used for treatment of disease conditions characterised by immunosuppression, eg. AIDS or AIDS-related complex, other virally or environmentally-induced conditions, and certain congenital immune deficiencies. The peptides can be employed to increase immune function which has been impaired by use of immunosuppressive drugs, such as certain chemotherapeutic drugs.
                                                                                                               08-JUN 1998 (first entry)
Yeast acylcoenzyme A:cholesterol acyltransferase-related enzyme II
Acylcoenzyme A:cholesterol acyltransferase; ACAT II;
ACAT related gene product 1; ARGP-1; ARP-2; sterol esterification;
ACAT related gene product 1; ARGP-1; ARP-2; sterol esterification;
ACAT related gene product 1; ARGP-1; ARP-2; sterol esterification;
ACAT related gene product 1; ARGP-1; ARP-2; sterol esterification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide fragments and analogues of CD26 and encoding nucleic acid - useful for stimulating immune response, e.g. for treatment of AIDS to counteract immunosuppressive drug, and as vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; T cell activation antigen; CD26; analogues; signal peptidase; immune-stimulating; response-stimimunosuppression; AIDS-related complex.
WO9745439-A1.
04-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adjuvant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MORIMOTO C, Schlossman WPI; 94-151317/18.
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R54614 standard; Protein; 593
                                                                                                          Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Delta594-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 islqwl
                                                                                                                                                                                                                                                                                                                          311 islqw1 316
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                                                                                                                                                                                                                                                                                           INLHWL
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                                                                                                                                                                                                                                                                                                                                                                                                                            593 AA;
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                                                                                                                                                                                                                                                                                                                                                      74.2%;
larity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                            cerevisiae.
                                             /note= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 593
                                                                               215..231
                                                                                                                                                                                                                         Protein; 642 AA.
                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Position of delta594-C deletion"
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66.78;
                         "transmembrane"domain"
                                                       "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INST INC.
Tanaka T;
                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 10; Le
Pred. No. 5.83e+02;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 8; I
Pred. No. 5.83e+02;
2; Mismatches C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; analogues; deletion; soluresponse-stimulating; AIDS
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                                                                                                                                                                                                                                                                                                                                                                                     Length 593;
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XEXAMPLE 1: Page 71-73: 111PF; ENGLISH.

YE YEAST ACY1-COENTRYME A:Cholesterol acy1transferase 2 (ARE2) is
C encoded by a gene (see T96370) located on chromosome X or XIV that
C was identified by homology to the human acy1-coenzyme A:cholesterol
C cy1transferase 1 gene (see T96368). ARE2 and ARE1 (see W38417)
C exhibit significant structural and functional homology to the
C putative catalytic component of cholesterol esterification in
C proteins is given in W38419. Deletion of the ARE1 and ARE2 genes
C produces a viable yeast cell with undetectable esterified sterol.
CC A claimed expression vector comprises a nucleic acid molecule
C encoding yeast wild type ARE1 or ARE2 operatively linked to a
CC promoter of RNA transcription. The vector and a claimed
C constructor system can be used for the recombinant production of
CC ARE2 inhibitors. ARE2 inhibitors can be used to treat
CC arteriosclerosis or hyperlipidaemia. ARE1 and ARE2 inhibitors can
CC also be used to inhibit fungal growth or to treat fungal invasion
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Best Local
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04-DEC-1997.

30-MAY-1996; US-657621.

30-MAY-1996; US-657621.

(UYCO ) UNIV COLUMBIA NEW YORK.

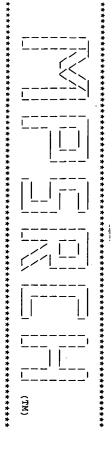
(INDV ) UNIV INDIANA FOUND.

Bard M, Sturley SL, Yang H;

WPI; 98-032644/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-1997; U09460.
30-MAY-1996; US-657620.
(UTCO ) UNIV COLUMBIA NE Sturley SL;
WPI; 98-032573/03.
N-PSDB; V01538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atherosclerosis or hyperilpidaemia
Disclosure; Fig 5C 1-3; 121pp; English.
This protein comprises yeast acylcoenzyme A:cholesterol
acyltransferaserelated enzyme II. The invention relates to
isolated nucleic acids (see V01533-35) coding for human and mous
acylcoenzyme A:cholesterol acyltransferase II and III (see
M43406-08), also designated ACAT related gene products (ARGP) 1
and 2. These can be used to identify inhibitors useful in the
treatment of atherosclerosis and hyperlipidaemia.
Sequence 642 AA;
ARE2 inhibitors. ARE2 inhibitors ca
arteriosclerosis or hyperlipidaemia,
also be used to inhibit fungal growt
(all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast acyl-coenzyme A:cholesterol acyltransferase 2. ARE2; yeast; Acyl-coenzyme A: cholesterol acyltransferase 2; ARE2; yeast; sterol; esterification; arteriosclerosis; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W38418 standard;
W38418;
                                                                                                                                                                                                                                                                                                                         Yeast acyl:coenzyme A:cholesterol acyl:transferase related and II - useful to identify inhibitor for treatment of hyperlipidaemia, arteriosclerosis and fungal invasion Example 1; Page 71-73; llipp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding acylcoenzyme A: cholesterol acyltransferase III - useful to identify inhibitors for treatment of
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Pred. No. 5.83e+02;
2; Mismatches C
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Query Match Similarity 66.74; Score 46; DB 28; Length 642;
Best Local Similarity 66.74; Pred. No. 5.83s+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 316 klbwl 321
Oy 51 FULHWL 56

Search completed: Tue Apr 20 14:07:03 1999
Job time: 16 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

abular output not generated. Tue Apr 20 14:06:10 1999; MasPar time 3.12 Seconds

Title:

Description:
Perfect Score:
Sequence: >US-08-836-455-1_1 (50-56) from trans.pep (2 of 3) 62 1 GINLHWL 7

Scoring table:

PAM 150 Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir58 1:pirl 2:pir2 3:pir3 4:pir4

Statistics: Mean 23.536; Variance 40.703; scale 0.578

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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V U U U U U U U U U U U U U U U U U U U	Score
85.55 85.55 85.55 86.66 80.66 80.66 80.66 80.66 80.66 80.66 80.66 80.66 80.66 80.66 80.66 80.66 80.66 80.66 80.66	. 0 .
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SSK1 protein - yeast SSK1 protein - yeast probable mmpL4 protein MADH dehydrogenase (u hypothetical protein probable tRNA delta(2 hypothetical protein probable tRNA delta(2 hypothetical protein probable tRNA delta(2 hypothetical protein protein transposase homolog transposase homolog transposase homolog transposase la la-associated cyclin adenovirus ELA-associated cyclin adenovirus ELA-associated cyclin adenovirus eLA-associated hypothetical protein protein protein lipopolysaccharide hypothetical protein probable thymidylate oligopeptide transportispenicillin N synth isopenicillin N synth	Description
3.77e+00 1.2.29e+01 2.6.47e+01 3.6.47e+01 6.47e+01 6.47e+01 6.47e+01 6.47e+01 6.47e+01 6.47e+01 6.47e+01 6.47e+01 6.47e+01 9.06e+01 9.06e+01 9.06e+01 1.26e+02 1.26e+02 1.26e+02	Pred. No.

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74.2	74.2	74.2	74.2	75.8	75.8	75.8	75.8	75.8	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4
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membrane p	envelope protein E (v	oligopeptide permease	sss protein - Pseudom	SOK1 protein - yeast	triacylglycerol lipas	hypothetical 44.7K pr	hypothetical protein	o O	RIC1 protein - yeast	hypothetical protein	reverse transcriptase	ന	small GTP binding pro	transferrin receptor	transferrin receptor	transferrin receptor	transferrin receptor	vsrA protein - Pseudo	tryptophanase (EC 4.1	ATP-gated ionchannel	rfbE protein - Salmon
	2.42e+02	2.42e+02	2.42e+02	1.75e+02	1.75e+02	1.75e+02	1.75e+02	1.75e+02	1.26e+02	1.26e+02	1.26e+02	1.26e+02	1.26e+02	1.26e+02	1.26e+02	1.26e+02	1.26e+02	1.26e+02	1.26e+02	1.26e+02	1.26e+02

ALIGNMENTS

Db 828 GIELHWL :	Query Match Best Local Similarity Matches 6; Conse	GENETICS #gene mmpL5 SUMMARY #length 96	##residues 1: ##cross-references	##status	#accession	#cross-referen	#journal #title				#authors	REFERENCE		ы
, 834 , 56 SSK1 protein - yeast (Saccharomyces cerevisiae)	93.5%; Score 58; DB 2; Length 964; larity 85.7%; Pred. No. 3.77e+00; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	mmpL5 #length 964 #molecular-weight 104784 #checksum 7944	##labe: :AL0219: D:g2909:	<pre>preliminary; nucleic acid sequence not shown; translation not shown</pre>	E70826	yenome sequence.	Nature (1998) 393:537-544 Deciphering the biology of Mycobacterium tuberculosis from	Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Squares, S.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.	Murphy, L.; Oliver, S.; Osborne, J.; McLean, J.; Moule, S.;	III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.;	Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,	E70826 A70500	<pre>#formal_name Mycobacterium tuberculosis 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998</pre>	E70826 #type complete probable membrane protein - Mycobacterium tuberculosis (strain H37RV)

1 = 1 = 1 = 1 =

Length 967;

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p_position 12R
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##cross-references EMBL:Z73178; NID:g1360295; PID:e245767; PID:g1360296;
##sexperimental_source strain S288C
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                                                                                                  Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Elgimeier, K.; Gas, S.; Barry III, C.E.; Tekata, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Sqares, R.; Sulston, J.E.; Taylor, K.; Whitchead, S.; Barrell, B.G.
                                                     Deciphering the biology of Mycobacterium tuberculosis the complete genome sequence. ICES MUID:98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       signal transduction
#superfamily response regulator homology
phosphoprotein; signal transduction; two-component regulatory
                                   C70831
                                                                                                                                                                                                                                                                                                                                                          A two-component system that regulates an osmosensing MAP kinase cascade in yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                   probable mmpL4 protein - Mycobacterium tuberculosis (strain
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#formal_name Saccharomyces cerevisiae
01-Aug-1995 #sequence_revision 24-May-1996 #text_change
06-Feb-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the Protein Sequence Database, May 1996
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$64742
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#binding_site phosphate (Asp) (covalent) #status
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Pred. No.
           nucleic acid sequence
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2.29e+01;
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#journal J. Mol. Biol. (1990) 212:599-634
#title Sequence and gene organization of the chicken mitochondrial
#cross-references MUID:90230301
#cross-references MUID:90230301
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Local Similarity 71.4%;
nes 5; Conservative
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Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M. Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shi S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabatta, S.
DNA Res. (1996) 3:109-136
Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequenc
                                                                                                                                                                                                                                                                   $75895 #type complete hypothetical protein - Syne formal_name Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #superfamily NADH dehydrogenase (ubiquinone) chain 4
membrane-associated complex; mitochondrion; NAD; oxidative
phosphorylation; oxidoreductase; respiratory chain
#length 459 #molecular-weight 51145 #checksum 1806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mitochondrion
SGC1
                                                                                                                                                                                                                            25-Apr-1997_#sequence_revision 25-Apr-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - chicken mitochondrion (SGC1) #formal_name mitochondrion Gallus gallus #common_name chicken 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mmpL4 #length 967 #molecular-weight 105233
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Pred. No. 3.;
2; Mismatcl
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2; NID:g12960; PID:g12970
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3.25e+01;
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Gaps

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sp.

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PCC 6803)

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Sequence

Length 459;

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#cross-references_MUID:97061201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors
                                                                                                                                                                                                                                                                                                                                                                              #gene
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##note the nucleottide sequence was submitted to the EMBL Data
Library, June 1996
                                                                                                                                                                                                                                             300 GVKIHWL 306
                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references GB:AE001238; GB:AE000520; NID:g3322928; PID:g3322935
##experimental_source strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type DNA
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Sutton, G.G.; Dodson, R.; Gwinn, M.; Hickey, E.K.; Clayton,
R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod,
M.P.; Salzberg, S.; Peterson, J.; Khalak, H.; Richardson,
D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDonald,
L.; Artiach, P.; Bowman, C.; Cotton, M.D.; Fujii, C.;
Garland, S.; Hatch, B.; Horst, K.; Roberts, K.; Watthey,
L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science (1998) 281:375-388
Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B71301 #type complete
probable tRNA delta(2)-isopentenylpyrophosphate transferase
(miaA) - syphilis spirochete
#formal_name Treponema pallidum subsp. pallidum #common_name
syphilis spirochete
24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                        TP0637 Hength 316 #molecular-weight 36174 #checksum
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B71301
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#length 495 #molecular-weight 54351 #checksum
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                                 #formal_name Mycobacterium:tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1
17-Jul-1998
                                                                                         B70661 #type complete in hypothetical protein Rv2337c - (strain H37RV)
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larity 71.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary; nucleic acid sequence
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                                                                                                                                                                                                                                                                                                     80.6%;
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Pred. No. 6.47e+01
3; Mismatches
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Pred. No. 4.60e+01;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not shown
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                                                     17-Jul-1998
                                                                                                            Mycobacterium
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Best Local Similarity 71.4%;
                                                                                       Matches
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Best Local Similarity
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#accession A70477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. #cross-references MUID:98295987
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#title
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##cross-references GB:Z83860; GB:AL123456; NID:g3261681; PID:e290744;
##Cross-references GB:Z83860; GB:AL123456; NID:g3261681; PID:e290744;
                                            342 GVKIHWL 348
                                                                                                                                                                                                                                                       ##mollecule_type DNA
##residues
1-476 ##label AQF
##cross-references GB.AE000770; NID:g2984274;
##experimental_source strain VF5
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50 GINLHWL 56
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                                                                                                                                                                                                                                                                                                                                                                                                                              Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;
Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.;
Keller, M.; Anjay, M.; Huber, R.; Feldman, R.A.; Short,
J.M.; Olson, G.J.; Swanson, R.V.
Nature (1998) 392:353-358
The complete genome of the hyperthermophilic bacterium
Aquifex aeolicus.
                                                                                                                                                                       #superfamily glutamate synthase small chain #length 476 #molecular-weight 52947 #chec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glutamate synthase small subunit gltD - Aquifex aeolicu:
#formal_name Aquifex aeolicus
08-May-1998 #sequence_revision 08-May-1998 #text_change
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#length 372 #molecular-weight 41272 #checksum
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                                                                                                                                                                                                                                                                                                                                            preliminary; nucleic acid sequence translation not shown
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translation not shown
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                                                                                         Score 50; DB 4, pred, No. 6.47e+01
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Pred. No. 6.47e+01
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#authors
Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.;
Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Weldman, J.M.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.;
Fujii, C.; Bownan, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.
Nature (1997) 388:539-547
#title The complete genome sequence of the gastric pathogen
Helicobacter pylori.
#cross-references MID:97394467
             CLASSIFICATION SUMMARY
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  ##molecule_type DNA
##cesidues 1-791 ##label TOM
##cross-references GB:AE000597; GB:AE000511; NID:g2314007; PID:g2314011;
##cross-references TIGR:HP0876
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TIGR:HI1478
#length 687 #molecular-weight 78719 #^^~~~~
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Local Similarity 83.3%;
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Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
Science (1995) 269:496-512
Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd.
#superfamily iron-regulated outer membrane protein #length 791 #molecular-weight 88525 #checksum 36
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09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
18-Sep-1998
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18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
24-Oct-1997
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Pred. No.
1; Misma
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Best Local Similarity
                                                                                                                                                                                                                                 #authors Steinhauer, W.R.; Walsh, R.C.; Kalfayan, L.J.
#journal Mol. Cell. Biol. (1989) 9:5726-5732
#title Sequence and structure of the Drosophila melanogaster ovarian
tumor gene and generation of an antibody specific for the
ovarian tumor protein.
#cross-references MUID:90066528
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                                                                                                                           #gene
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Nucleic Acids Res. (1989) 17:3304

#journal Nucleotide sequence of a cDNA from the putative ovarian tumor

#title locus of Drosophila.melanogaster.

#cross-references MUID:89263747
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                                                                                                                                                       ##status preliminary
##molecule_type DNA; mRNA
##residues 1-811 ##label
##cross-references GB:M30825;
 593 GVDLHW 598
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Y #length 811 #molecular-wei
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                                             y Match 80.6%;
Local Similarity 66.7%;
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#cross-references EMBL:X13693; NID:g8315; PID:g8316
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#length 811
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ovarian tumor protein - fruit fly (Drosophila melanogaster)
#formal_name Drosophila melanogaster
23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change
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07-Jun-1990 #sequence_revision 07-Ju
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nor locus protein - fruit fly (Drosophila
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                                                                                         #molecular-weight 92612 #checksum
                           Score 50; DB 2; 1
Pred. No. 6.47e+01;
2; Mismatches (
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NID:g158028; PID:g158029
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#map_posttion 16q12.2-16q12.2
CLASSIFICATION #superfamily retinoblastoma-associated protein
SUMMARY #length 1082 #molecular-weight 122475 #checksum
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                                                                                                                                                                                                                                                                                                                                                                                                      #authors Hannon, G.J.; Demetrick, D.; Beach, D.
#journal Genes Dev. (1993) 7:2378-2391
#title Isolation of the Rb-related p130 through its interaction with
#cross-references MUID:94074896
#cross-references MUID:94074896
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#title Cloning of a new member of the retinoblastoma
#tothe Cloning of a new member of the retinoblastoma
#tothe Cloning of a new member of the retinoblastoma
#cross-references_MUID:93368960
                                                                                                                                                                                                                                                                                                                                                                                      #accession
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#residues 1-1082 ##label RES
##cross-references EMBL:X74594; NID:g397147; PID:g397148
                                                                                                                                                                                                                                                           ##status preliminary

##mollecule_type mRNA
##residues 1-1139 ##label HAN
##cross-references GB:S67171; NID:g453131; PID:g453132
##experimental_source HeLa S3 suspension cells
##experimental_source with a suspension cells
##experimental_source MCBIP:140577)
##note Scauches with a suspension NCBI backbone (NCBIN:140576,
##note NCBIP:140577)
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Rb2/p130 protein - human
#formal_name Homo sapiens #common_name man
06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
29-Aug-1997
                                                                                                                                                                                                                       A49370
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E1A-associated cyclin-binding protein p130 -
#formal_name Homo sapiens #common_name man
07-Apr-1994 #sequence_revision 18-Nov-1994 #t
20-Mar-1998
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larity 71.4%;
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#type complete
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1; Mismatches 1
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Matches
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#journal
#title
                                                                                                                                                                                             #accession A49369
##status pre!
##molecule_type mRNA
##residues 1-11
                                                                                                                                       ##residues 1-1139 ##label LIA
##cross-references GB:X76061
FICATION #superfamily retinoblastoma-associated
# length 1139 #molecular-weight 128451
                               81 GNDLHWL
50 GINLHWL 56
                                                                                     Similarity
                                                                                                                                                                                                                                                             Li, Y.; Graham, C.; Lacy, S.; Duncan, A.M.V.; Whyte, P. Genes Dev. (1993) 7:2366-237
The adenovirus Elha-associated 130-kD protein is encoded by member of the retinoblastoma gene family and physically interacts with cyclins A and E.
                                                                                                                                                                                                                                                                                                                                                                                           adenovirus ElA-associated 130k protein - human formal_name Homo sapiens #common_name man 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 03-May-1996
                                                                    Conservative
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                                                                                 80.68;
71.48;
                                                                                   Score 50; DB 2; I
Pred. No. 6.47e+01;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Tue Apr 20 14:04:55 1999; MasPar time 2.51 Seconds 74.986 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-836-455-1_1 (50-56) from trans.pep (2 of 3) 62 1 GINLHWL 7

Scoring table:

PAM 150 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot35 1:swissprot

Database:

Statistics: Mean 24.102; Variance 35.768; scale 0.674

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score Match Length DB ID Description Pred. No.	22 23	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ.	ъ	4	ω	N	<u>بر</u>	sult No.
Length DB ID SSKI_YEAST OSOMOLARITY TWO-COMPON 7.1033 1 YDK9_SCHPO HYPOTHETICAL 116.5 KD 7.459 1 NUAM_CHICK NADH-UBIQUINONE OXIDOR 1.459 1 YFM_CAEEL HYPOTHETICAL 166.0 KD 1.459 1 YFM_CAEEL HYPOTHETICAL 166.0 KD 1.459 1 YFM_CAEEL HYPOTHETICAL 166.0 KD 1.459 1 REL2_HUMAN EXINOBLASTOWA-LIKE PR 2.1610 1 RPC1_BP186 REPERSSOR PROTEIN CI. 3.192 1 RPC1_BP186 REPERSSOR PROTEIN CI. 3.2 KD 9.361 1 YNO2_PARDE HYPOTHETICAL 22.9 KD 9.361 1 YNO3_CEPAC 11COPEPTIDE TRANSPORT 4.379 1 PEX6_RAT 1 INS_CEPAC 11COPETIDE TRANSPORT 4.379 1 PEX6_RAT 1 TOWALECOLI CIP-TYVELOSE-2-EPIMERA 4.379 1 PEX6_RAT 1 TOWALECOLI TRATFORDHANASE (EC 4.1.471 1 TNAA_ECOLI TRATFORDHANASE (EC 4.1.471 1 TNAA_ECOLI TRANSFERRIN RECEPTOR 4.471 1 TNAA_ECOLI TRANSFERRIN RECEPTOR 4.471 1 TNAA_ECOLI TRANSFERRIN RECEPTOR 4.471 1 TYAFP_RHISN PROTEIN FROM 2.410 1 Y4FP_RHISN PROBABLE ABC TRANSPORT 4.410 1 Y4FP_RHISN PROBABLE ABC TRANSPORT 7.901 1 SOK1_YEAST SOK1_PROTEIN 7.7 ND 9.75 1 NRTB_SYNY3 NITRATE TRANSPORT PERM 1.	46	47	. 47	47	48	48	48	48	48	48	4.8	. 48	49	49	49	50	50	51	51	52	53	53	Score
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Pred. No. 7.08e+00 7.08e+00 7.08e+01 1.55e+01 1.55e+01 2.29e+01 2.29e+01 3.34e+01 3.34e+01 4.87e+01 4.87e+01 4.87e+01 4.87e+01 4.87e+01 7.04e+01 7.04e+01 7.04e+01 7.04e+01 7.04e+01 7.04e+01 7.04e+01 7.04e+01 7.04e+01	TRANSPORT	44.7 KD		PROTEIN			TRANSFERRIN RECEPTOR P	(EC 4	σ	CDP-TYVELOSE-2-EPIMERA	ISOPENICILLIN N SYNTHE		63.2 KD	22.9					()		116.5		Description
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634 VNLHWL 639 :||||| 51 INLHWL 56

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YQK4_CAEEL	AMY2_SALTY	FUCK_HAEIN	YGGS_HAEIN	YQIE_HAEIN	QA1S_NEUCR	DPP4_RAT	DPP4_HUMAN	DPP4_MOUSE	ARE2_YEAST	HEMA_IAHC6	HEMA_IAHPR	HEMA_IASTA	HEMA_IAFPW	HEMA_IACKV	HEMA_IAFPR	HEMA_IATKR	YCR2_ERWHE	POLG_DEN23	NU4M_STRCA	OXDA_TRIVR	OPPB_SALTY
HYPOTHETICAL 64.3 KD P	CYTOPLASMIC ALPHA-AMYL	L-FUCULOKINASE (EC 2.7	HYPOTHETICAL PROTEIN H	HYPOTHETICAL PROTEIN H	QUINATE REPRESSOR.	DIPEPTIDYL PEPTIDASE I	DIPEPTIDYL PEPTIDASE I	DIPEPTIDYL PEPTIDASE I	STEROL O-ACYLTRANSFERA	HEMAGGLUTININ PRECURSO	HYPOTHETICAL PROTEIN I	GENOME POLYPROTEIN (MA	NADH-UBIQUINONE OXIDOR	D-AMINO ACID OXIDASE (OLIGOPEPTIDE TRANSPORT						
1.45e+02	1.45e+02	1.45e+02	1.45e+02	1.45e+02	1.01e+02	1.01e+02	1.01e+02	1.01e+02	1.01e+02	1.01e+02	1.01e+02	1.01e+02	1.01e+02	1.01e+02	1.01e+02	1.01e+02	1.01e+02	1.01e+02	1.01e+02	1.01e+02	1.01e+02

ALIGNMENTS

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8e+00 es	85.5%: Score 53: DB 1:	SQ SEQUENCE /12 AA; /8529 MW; 24AU5B5F CRC32;	CONFLICT 181 181 P -> S (IN	MUTAGEN 554 554 D->N: ACTIVATES.	MOD_RES 554 554 PHOSPHORYLATION	DOMAIN 501 646 RECEIVER DOMAIN	SENSORY TRANSDUCTION	SGD; L0002084;	EMBL; Z73178; E245767;	EMBL; L26523; G496306;	-1- SIMILARITY: TO PROKARYOTE SENSORY	CC -1- SUBCRITITIAR LOCATIONS CYTOTERATIO CONTENTIALLY.	PHOSPHORYLATION BY SENT.	MAPK CASCADE. IN LOW-OSMOLARITY MEDIA, IS	SSK2 AND SSK22, TWO MAPKKKS THAT FURTHER	PBS2->HOG1 PATHWAY. THE UNPHOSPHORYLATED		SLN1/SSK1 ACTIV		SUBMITTED (MAY-1996) TO EMBL/	VANDENBOI		3	RA MAEDA T., WURGLER-MURPHY S.M., SAITO H.; RL NATURE 369:242-245(1994).	MEDLINE; 9			OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).		OSOMOLARITY TWO-C	01-NOV-1997 (REL.	01-NOV-1997 (REL. 35,	Q07084; Q07909; ·	RESULT 1 ID SSK1_YEAST STANDARD; PRT; 712 AA.
Indels	Lenath 712:				(PROBABLE).	(POTENTIAL).					PROTEINS		•	INHIBITED TH	JLATE THE	FORM OF SSK1 ACTIVATES	S THE SS	ITY OF THE	ATORY SYSTEM	iks.														
0; Gaps														THROUGH T	PBS2-H	ACTIVAT	SSK2/SSK22->	[2]	TEM															
ps 0;														THE	061	ES	2->																	

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OI-NOV-1997 (REL. 35, OI-NOV-1997 (REL. 35, GLYCEROL KINASE (EC 2) (GLYCEROKINASE) (GK).
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Best Local (
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Best Local
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                                                                                                          GLPK_SYNY3
P74260;
01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                   P18939;
01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MITOCHONDRION.
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GALLUS (CHICKEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BADCOCK K., CHURCHER C.M., WOOD V., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-- SIMILARITY: TO YEAST YNL132W AND AN A.AMBISEXUALIS HYPOTHETICAL
PROTEIN (AC 954008).

EMBL; 295334; E315494;
HYPOTHETICAL PROTEIN; ATP-BINDING.
NP_BIND 282 289 ATP (POTENTIAL).
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SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
SCHIZARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOM
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P87115;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDA
HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C
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les 5; Conse
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                                                                     .. 35, CREATED)
.. 35, LAST SEQUENCE UPDATE)
.. 35, LAST ANNOTATION UPDATE)
(EC 2.7.1.30) (ATP:GLYCEROL 3
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83.3%;
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2; M
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Pred. No. 7
1; Mismat
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                                                                          3-PHOSPHOTRANSFERASE)
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Best Local Similarity
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Best Local s
Matches
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P10383;

01-MAR-1989 (RI

01-MAR-1989 (RI

01-NOV-1991 (RI

OVARIAN TUMOR I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
PRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YF1M_CAEEL
Q21874;
15-JUL-1998
15-JUL-1998
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ-1-SIMILARITY: STRONG, TO C.ELEGANS F54D1
EMBL; 270287; E233847; -.
WORMPEP; ROSELO.5; CEO5287.
HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
SEQUENCE 1459 AA; 165994 MW; 46E17445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYCEROKIMASE, J. EMBL; D90913; G1653440; -. PROSITE; PS00933; FGGY_KINASES_1; FALSE_NEG. PROSITE; PS00445; FGGY_KINASES_2; 1. GLYCEROL METABOLISM; TRANSFERASE; KINASE. S4351 MW; C7247592 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MATTHEWS L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL R09E10.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              640 ISLHWL 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OKUMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A.,
YASUDA M., TABATA S.,
DNA RES. 3:109-136(1996).
-!- CATALYTIC ACTIVITY: ATP + GLYCEROL = ADP + GLYCEROL 3-PHOSPHATE.
-!- PACHWAY: RATE-LIMITING STEP IN GLYCEROL UTILIZATION.
-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-!- SUBUNIT: BELONGS TO THE FUCOKINASE / GLYCEROKINASE / XYLULOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 GTKLHWL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KANEKO I., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA I., HOSOUCHI I., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S., SHIMPO S., TAKEUCHI C., WADA I., WATANABE A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYNECHOCYSTIS SP. (STRAIN PCC 6803).
PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
CYANOBACTERIA (BLUE-GREEN ALGAE); CHROOCOCCALES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 INLHWL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 97061201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 GINLHWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                           (REL. 10, CREATED)
(REL. 10, LAST SEQUENCE UF
(REL. 20, LAST ANNOTATION
OR LOCUS PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REL. 3
(REL. 3
(REL. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36, CREATED)
36, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
0 KD PROTEIN R09E10.5 IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.3%;
71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GENBANK/DDBJ DATA BANKS
TO C.ELEGANS F54D1.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51;
Pred. No.
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Pred. No. 1.55e+01;
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                                                                                                                                                         ON UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .55e+01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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DROSOPHILA EUKARYOTA; [1]

METAZOA;

ARTHROPODA;

INSECTA; DIPTERA

MELANOGASTER (FRUIT FLY)

DIO

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RESOLUTION OF THE RESOLUTION O
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Matches
                                                                                                      Query Match
Best Local
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                                                                                  Matches
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EMBL; M30825; G158029; -.
PIR; S04085; S04085.
PIR; A33829; A33829;
FLYBASE; FB900003023; otu.
CONFLICT 300 300
CONFLICT 789 789
                                                                                                                                                              PHOSPHORYLATION; ANTI-ONCOGENE.

DOMAIN 360 967 POCI

DOMAIN 360 559 DOM

DOMAIN 560 770 SPAY

DOMAIN 771 967 DOM

SEQUENCE 1082 AA; 122476 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=CANTON-S; MEDLINE; 89263747. CHAMPE M.A., LAIRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SCOUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
RETINOBLASTOMA-LIKE PROTEIN 2 (130 KD RETINOB
PROTEIN) (PRB2) (P130).
                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 93368960.

MAYOL X., GRANA X., BALDI A., SANG N., HU Q., GIORDANO A.;

ONCOGENE 8:2561-2566(1993).

-!- FUNCTION: MAY HAVE A FUNCTION IN CELL CYCLE REGULATION. BINDS TO AND MAY BE INVOLVED IN THE TRANSFORMING CAPACITY OF THE ADENOVIRUS E1A PROTEIN. MAY ACT AS A TUMOR SUPPRESSOR. POTENT INHIBITOR OF E2F-MEDIATED TRANS-ACTIVATION, ASSOCIATES PREFERENTIALLY WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA;
EUTHERIA; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMO SAPIENS (HUMAN),
HOMO SAPIENS (HUMAN),
HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STEINHAUER W.R., WALSH R.C., KALFAYAN L.J.;
MOL. CELL. BIOL: 9:5726-5732(1989).
-i- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR FEMALE FERTILITY.
-i- SIMILARITY: LOW, WITH THE DROSOPHILA BAG-OF-MARBLES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                           ++
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEIC
                                                                                                                                                                                                                                                                                          TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593 GVDLHW 598
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                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: NUCLEAR. SIMILARITY: BELONGS TO THE RET
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  GINLHWL
                                       GNDLHWL 30
                                                                                                                                                                                                                                                                                                                                     X74594; G397148;
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                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          811 AA;
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llarity 66.7%;
Conservative
                                                                              80.6%;
larity 71.4%;
Conservative
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S RES. 17:3304-3304(1989).
  56
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789
92616
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                                                                                                                                                              POCKET (BINDS E1A).
DOMAIN A.
SPACER.
DOMAIN B.
DOMAIN B.
MW; 4F714AE5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                Pred.
1; 1
                                                                                                                         Score
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) -> P (IN

B8C8AC5D
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                                                                                re 50; DB 1; Len
1. No., 2.29e+01;
Mismatches 1;
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2.29e+01;
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CRC32;
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                                                                                                                       Length 1082;
                                                                                                                                                                                                                                                                                                                                                       PROTEIN
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                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                       (RB) FAMILY
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RESULT
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RPC1_BP186
P08707:
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YNQ2_PARDE
P29908;
P1-APT
   YD89_SCHPO
Q10414;
Q1-OCT-1996
Q1-OCT-1996
Q1-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XU X., MATSUNO-YAGI A., YAGI T.;
BIOCHEMISTRY 30:8678-8684(1991).
-I- FUNCTION: URF2 PRODUCT MAY BE INVOLVED IN THE TRANSFER OF IRON-
SULFUR CLUSTERS TO THE NADH DEHYDROGENASE COMPLEX. IT MAY ALSO
BE REQUIRED FOR THE ASSEMBLY OF THE NADH DEHYDROGENASE COMPLEX.
-I- SIMILARITY: SIGNIFICANT TO ORF3 OF P.DENITRIFICANS (LOCATED
BETWEEN THE COX11 & COX111 GENES).
EMBL; M74171; G150604; -
PIR; B40296; B40296.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
HYPOTHETICAL 22.9 KD PROTEIN IN NGO2 3'REGION
PARACOCCUS DENITRIFICANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1988 (REL.
01-JAN-1988 (REL.
01-FEB-1995 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 13548;
MEDLINE; 91363357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACTERIOPHAGE 186.
VIRIDAE; DS-DNA NONENVELOPED VIRUSES; MYOVIRIDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNCERTAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPRESSOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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                                                                                                                                                                                                                                   GI-NLHWL
                                                                                                                                                                                                                                                                    GIGDLHWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GANLOWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GINLHWL
                                                                                                                                                                                                                                                                                                                                                   Similarity 75.0% 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 71.48, 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRACILICUTES;
   (REL.
(REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
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                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CI,7,6,6
34, CREATED)
34, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.08;
71.48;
                                                                                                                                                                                                                                                                                                                                                                           79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22906 MW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPRESSOR; DNA-BINDING MW; 7D8E003E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCOTOBACTERIA; AEROBIC RODS AND
                                                                                                                                                                                                                                                                                                                                                Score 49;
Pred. No.
1; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49;
Pred. No.
1; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DA6A9F8A CRC32;
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3.34e+01
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3.34e+01;
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Best Local
ECGGENE; EG10675; OPPB.

ECGGENE; EG10675; OPPB.

PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.

TRANSPORT; PEPTIDE TRANSPORT; TRANSMEMBRAN
DOMAIN

1 9 CYTOPLASMIC (
TRANSMEM 10 30 PROBABLE
DOMAIN

31 99 EXTRACELLULAF
TRANSMEM 100 121 PROBABLE.
                                                                                                                                                                                             KASHIWAGI K., YAMAGUCHI Y., SAKAI Y., KOBAYASHI H., IGARASHI K.;
J. BIOL. CHEM. 265:8387-8391(1990).

-!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR OLIGOPEPTIDES; PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.

-!- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-PROTEIN_DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPPBC
                                                                                                                        EMBL; AE000223; G1787497; -
EMBL; D90763; G1742033; -
EMBL; D90852; D1016767; -
EMBL; J05433; -; COT_ANNOTATED_CDS.
                                                                                                                PIR; B36263; B36263
                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-16 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T., IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KAMAI K., KASAI H., KASHIMOTO K., KIM S., KINURA S., KITAGAWA M., KITAKAWA M., MAKINO K., MASUDA S., MIKI T., MIZOBUCHI K., MORIHIH., MOTOMURA K., NARAMURA Y., WASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.; SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPPB_ECOLI STANDARD;
P31132; P76026; P77550;
01-JUL-1993 (REL. 26, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35 TAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
BLATTNER F.R., PLUNKETT
SUBMITTED (JAN-1997) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V., SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

I'S SIMILARITY: TO YEAST YGR093W.

EMBL; 270690; E234475; -.

HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENTEROBACTERIACEAE
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SPAC1F3.09.
SCHIZOSACCHAROMYCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; FUNGI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                561 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ES POMBE (FISSION YEAST).
ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ğ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G. III, MAYHEW G.F., PERNA N.T., EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                 PROBABLE:
EXTRACELLULAR (PROBABLE)
                                           TRANSMEMBRANE; INNER M. CYTOPLASMIC (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; DB 1;
No. 3.34e+01
                                                                                                                                                                 , -
, .
                                                              INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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                                                Query Match
Best Local (
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PIR; A24567; A24567.

PIR; A23955; A23955;

PIR; S03312; S03312.

PROSITE; PS00185; IPNS_1; 1.

PROSITE; PS00186; IPNS_2; 1.

PROSITE; PS00186; IPNS_2; 1.

PROSITE; PS00186; IPNS_2; IRNS_2; IRNS_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local s
Matches
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01-FEB-1995 (REL. 05, LAST SEQUE
01-FEB-1995 (REL. 31, LAST ANNOT,
ISOPENICILLIN N SYNTHETASE (IPNS)
PCBC OR IPS.
CEPHATOROMOTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 40-78 AND 237-264, AND PHOTOAFFINITY LABELLING.
MEDLINE; 90197638.

BALDWIN J.E., COATES J.B., MOLONEY M.G., PRATT A.J., WILLIS A.C.;
BIOCHEM. J. 266:561-567(1990).

-I- CATALYTIC ACTIVITY: REMOVES, IN THE PRESENCE OF OXYGEN, 4 HYDROGEN ATOMS FROM L-(ALPHA-AMINOADIPYL)-L-CYSTEINYL-D-VALINE TO FORM THE AZEITINONE AND THIAZOLIDINE RINGS OF ISOPENICILLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ++
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FEBS LETT. 188:253-256(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 3-52.
STRAIN-ATCC 60777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKATRUD P.L., VANFRANK R.M., INGOLIA T.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAMSON S.N., BELAGAJE R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEPHALOSPORIUM ACREMONIUM (ACREMONIUM CHRYSOGENUM).

EUKARYOTA; FUNGI; ASCOMYCOTINA; PLECTOMYCETES; EUROTIALES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 86040479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPNS_CEPAC P05189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 GINLHWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZETIDINONE AND THIAZOLIDINE RINGS OF COFACTOR: IRON AND ASCORBATE. PATHWAY: CENTRAL ROLE IN THE BIOSYNTHE
                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                    OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CEPHALOSPORIN.
                                             Similarity
                     4;
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306
                  Conservative
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                                    Score 48; DB 1;
Pred. No. 4.87e+01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE BIOSYNTHESIS OF
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Pred. No. 4.87e+01
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                                                                                                                          -> T (IN REF. 2
EE264220 CRC32;
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CYTOPLASMIC
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      Mismatches
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(E.P., E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UPDATE)
                                                                                                                                                        IRON; V
REF. 2).
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                                                             Length
                                                                                                                                                                                 VITAMIN
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      Indels
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Best Local S
Matches
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VERMA N., REEVES P.R.;
J. BACTERIOL. 171:5694-5701(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RFBE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ol-JAN-1990 (REL. 13, CREATED)
O1-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
O1-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
CDP-TYVELOSE-2-EPIMERASE (EC 5.1.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFBE_SALTI
P14169;
                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
P2X PURINOCEPTOR 6 (ATP RECEPTOR) (P2X6) (PURINERGIC RECEPTOR).
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PROKARYOTA; GRACILICUTES;
                                                                                                                                                              MEDLINE; 96264662.
SOTO F., GARCIA-GUZMAN
BIOCHEM. BIOPHYS. RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIPOPOLYSACCHARIDE BIOSYNTHESIS; SEQUENCE 338 AA; 37958 MW; 1
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                                                                                                                                                                                                                         STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                     MEDLINE; 96256686.
COLLO G., KAWASHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REEVES P.R.;
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                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              SURPRENANT A., BUELL G.N.;
J. NEUROSCI. 16:2495-2507(1996).
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE-CERVICAL GI
                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATTUS NORVEGICUS (RAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
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               SUBCELLULAR LOCATION: 1
SIMILARITY: BELONGS TO
L; X92070; E205329; -.
L; X97376; E242827; -.
                                                                             CHANNEL.
SUBUNIT: HOMO- OR HETEROPOLYMERS (BY SIMILARITY).
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                                                                                                                                            FUNCTION: RECEPTOR
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Similarity 100.0%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                       KAWASHIMA E., PICH E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 GANGLION;
P2X_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHORDATA;
                                                                                                                                 M., KARSCHIN C., STUEHMER W.;
COMMUN. 223:456-460(1996).
FOR ATP THAT ACTS AS A LIGAND
                                                         INTEGRAL
O THE P2X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
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Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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12C22DD0 CRC32;
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                                                         MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Lens
. 4.87e+01;
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REFERENCE REPRESENTATION OF THE PROPERTY OF TH
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Best Local S
Matches
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BURLAND V.D., press
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DOMAIN
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21-JUL-1986
01-JUL-1993
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CARBOHYD
                                                                                                                                                                                            MEDLINE; 860
STEWART V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                            SEQUENCE OF 1-12.
STRAIN-K12 / EMG2;
LINK A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-B/1T7-A;
MEDLINE; 89323226
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MEDLINE; 82007678.
DEELEY M.C., YANOFSKY C.;
J. BACTERIOL. 147:787-796(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESCHERICHIA COLI.
PROKARYOTA; GRACILI
ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRYPTOPHANASE
TNAA OR IND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOKUSHIGE M., TSUJIMOTO N.,
YAMAMOTO M., KIM E.H., HIRA
BIOCHIMIE 71:711-720(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                               J. BACTERIOL.
                                                                                                                         SEQUENCE OF 463-471 FROM N.A. MEDLINE; 91216998.
                                                                                                                                                                                                                            STRAIN-K12;
                                                                                                                                                                                                                                                                                         MEDLINE; 72134434.
KAGAMIYAMA H., MAT
                                                                                                                                                                                                                                                                                                                           STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        GENOMICS
               SUBMITTED (OCT-1994)
                                                                                                             SARSERO
                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                          J. BIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                             BACTERIOL.
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                                                                                                           J.P.,
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                                                                                                                                                                                                                                           OF 1-21
                                                                                                                                                                                                                                                                            CHEM.
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                                                                                                                                                                                                                                                                                                                                                                        V.D., PLUNKETT G.
16:551-561(1993)
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379
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L. 164:731-740(1985).
                                                                                                                                                                                                                                                                                                                                        TRYPTIC PEPTIDES
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                                                                                              WOOKEY P.J., GOLLNICK
173:3231-3234(1991).
                                                                                                                                                                                                                                                                          MATSUBARA H., SNELL
247:1576-1586(1972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEMBRANE;
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                                                                                                                                                                                                                                             FROM
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26, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
4.1.99.1) (L-TRYPTOPHAN INDOLE-LYASE) (TNASE).
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42450
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379
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83.3%;
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                                                                                                                                                                                                                                             N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIRAGI Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z
               THE SWISS-PROT DATA BANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANCE
                                                                                                                                                                                                                                                                                                                                                                                       III,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC POTENTIAL.
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1 (POTENTIAL).
EXTRACELLULAR, C
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; BB28C0D0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                re 48; DB 1; 1
1. No. 4.87e+01
Mismatches
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                                                                                                           P.D.,
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                                                                                                             YANOFSKY C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYSTEINE-RICH
                                                                                                                                                                                                                                                                                                                                                                                       BLATTNER
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                                                                                                             PITTARD A.J.;
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Search completed: Tue Apr 20 14:05:02 1999 Job time: 7 secs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND SEKIND;
C -I- CORACTOR: PYRIDOXAL PHOSPHATE.
C -I- SUBUNIT: HOMOTETRAMER.
C -I- SUBUNIT: HOMOTETRAMER.
C -I- SUBUNIT: HIGH, TO TYROSINE PHENOL-LYASE.
EMBL; KX00032; G147997; -
EMBL; KX00032; G147997; -
EMBL; XL5974; G41936; -
EMBL; XL5974; G418001; -
EMBL; H1990; G148001; -
EMBL; H1990; G148001; -
EMBL; H10328; G290556; ALT_INIT.
EMBL; H10328; G290556; ALT_INIT.
EMBL; AE000448; G1790144; ALT_INIT.
EMBL; AE000448; G1790144; ALT_INIT.
EMBL; AE00048; G1790144; ALT_INIT.
EMBL; AE00048; G1790144; ALT_INIT.
EMBL; AE00048; G1790144; ALT_INIT.
EMBL; B0103; TIPL.
ECOZENB; EG11005; TNAA.
ECOZENB; EG11005; TNAA.
ECOZENB; EG11005; TNAA.
FROSITE; PS00853; BETA_ELM_LYASE; 1.
ECOZENB; EG11005; TNAA.
FROSITE; PS00853; BETA_ELM_LYASE; 1
ECOZENB; EG11005; TNAA.
FROSITE; TNAAA.
FROSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 77.4%; Score 48; DB 1; Length 471; Best Local Similarity 71.4%; Pred No. 4.87e+01; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                 325 GMNLDWL 331
|:|| ||
50 GINLHWL 56
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MEDLLIPS, 89278130.

PHILLIPS R.S., GOLLNICK P.D.;

J. BIOL. CHEM. 264:10627-10632(1989).

-i- CATALYTIC ACTIVITY: L-TRYPTOPHAN + H(2)O = INDOLE + PYRUVATE + NH(3) (ALSO CATALYZES THE SYNTHESIS OF TRYPTOPHAN FROM INDOLE AND SERINE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp in on: protein - protein database search, using Smith-Waterman algorithm Tue Apr 20 14:05:20 1999; MasPar time 4.35 Seconds 80.112 Million cell updates/sec

Description: Perfect Score: Title: >US-08-836-455-1_1 (50-56) from trans.pep (2 of 3) 62 1 GINLHWL 7

abular output not generated.

Scoring table:

Sequence:

PAM 150 Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

isp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 23.380; Variance 35.189; scale 0.664

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11111111111111111111111111111111111111	Result
0 9 8 7 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	t Score
77778888888888888888	Query Match I
964 2 964 2 198 2 372 198 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Length DB
053784 P731731 P95233 Q60260962 Q2109962 Q2109962 Q250198 Q550198 Q550198 Q150081 Q150081 Q150081 Q150132 Q551123 Q551123 Q551123 Q551123 Q551123 Q551123	Ħ
PUTATIVE MEMBRANE PROT PUTATIVE TRANSMEMBRANE INTE, REGA, GEPA, GEPB INTE, REGA, GEPA, GEPB HYPOTHETICAL 41.3 KD P CARCINOEMBRYONIC ANTIG RO9D1.3. GLUTAMATE SYNTHASE SMA TRANSPOSASE A (MUA). TONB-DEPENDENT RECEPTO IRON-REGULATED OUTER M RETINOBLASTOMA-LIKE 2 P130. P130. P130. P130. 130K PROTEIN. 130K PROTEIN. 15PODIFICANSFERASE I. LIPOOLIGOSACCHARIDE HEE 1.5 HEPTOSYLTRANSFERAS SUCCINYLGLUTAMATE DESU HYPOTHETICAL 42.6 KD P K08F8.1.	Description
1.45e+00 1.15e+01 1.45e+01 1.5e+01 1.5e+01 1.6 3.74e+01 1.6 3.74e+01 1.7 3.7 4e+01	Pred. No.

0

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
47	47	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	49	49	49	49
75.8	75.8	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	79.0	79.0	79.0	79.0
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073626	061669	Q04135	Q24335	Q18423	Q12830	Q62351	207891	Q92199	Q99376	Q82511	Q52558	Q22675	035789	Q00047	017940	Q59537	062113	Q66496	059366	017882	Q48727	P71448	Q93382	Q23616
₹.	SELECTIN 1 (FRAGMENT).	PUTATIVE RNA-DIRECTED	REVERSE TRANSCRIPTASE.	HYPOTHETICAL PROTEIN C	FETAL ALZ-50-REACTIVE	TRANSFERRIN RECEPTOR.	TRANSFERRIN RECEPTOR P	PUTATIVE TRANSPOSASE.	TRANSFERRIN RECEPTOR P	HEMAGGLUTININ PRECURSO	VSRA.	T22C8.2.	GLYCOPROTEIN SPECIFIC	ISOPENICILLIN N SYNTHE	K08F9.3.	LIPASE-ESTERASE (EC 3.	C47F8.4.	STRAIN NE89 ORF2.	205AA LONG HYPOTHETICA	F49C5.5.	BETA-GALACTOSIDASE.	BETA-D-GALACTOSIDASE.	HYPOTHETICAL PROTEIN C	ZK822.5.
1.17e+02					8.03e+01	8.03e+01	8.03e+01	8.03e+01	8.03e+01	8.03e+01	8.03e+01		8.03e+01	8.03e+01	8.03e+01	8.03e+01	8.03e+01	8.03e+01	8.03e+01	8.03e+01	5.49e+0	5.49e+01	5.49e+0:	5.49e+01

ALIGNMENTS

RESULT ID O AC O DT 0	Db Qy	RA CORE EN SQ SI SQ SI SQ SI SQ SI Sest	R R R R R R R	R R R R R	R R R R R	0 0 g g	2000;	RESULT
JT 2 053735 PRELIMINARY; PRT; 967 AA. 053735; 01-JUN-1998 (TREMBLREL. 06, CREATED)	GIELHWI 834	LE S.T.; NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996). MBL; AL021943; E1253102; EQUENCE 964 AA; 104784 MW; BA29E3A3 CRC32; MATCh 93.5%; Score 58; DB 2; Length 964; Local Similarity 85.7%; Pred. No. 1.45e+00; Local Similarity 85.7%; Pred. No. 1.45e+00; Local Similarity 85.7%; Pred. No. 1.45e+00; Local Similarity 85.7%; Pred. No. 1.45e+00;		SEQUENCE FROM N.A. STRAIN-H37RV; COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.; SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.	SEQUENCE FROM N.A. STRAIN-H37EV; HAMLIN N., CHURCHER C.M.; SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.	MTV040.045. MTV040.045. MYCOBACTERIUM TUBERCULOSIS. PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.	01-JUN-1998 (TREMBLREL. 06, CREATED) 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE) 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE) DUTATIVE MEMBARIL DOCTETU	LT 1 053784 PRELIMINARY; PRT; 964 AA.

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RESULT
ID P9
AC P9
DT 01
MM
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ID 971161
AC 971161;
DT 01-FEB-1997 (
DT 01-FEB-1997 (
DT 01-AUG-1998 (
DE INTB, REGA, G
GN GEPB,
OS BACTEROIDES N
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Best Local S
Matches
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      P95233;
P95233;
01-MAY-1997 (
01-MAY-1997 (
01-MAY-1997 (
HYPOTHETICAL
                                                                                                                                                                                                      BLOOMFIELD G.A., WHITTLE G., MC MICROBIOLOGY 143:553-562(1997).
EMBL; X98546; E288655; -...
                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                 BACTEROIDES NODOSUS (DICHELOBACTER NODOSUS) PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AN
                                                                                                                               157 ITLHWL 162
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           BACTEROIDACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROC. NATL. ACAD. SCI. U.S.A. EMBL; AL021932; E1252519; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHILIPP W.J., POULET S., EIGLMEIER K., BALASUBRAMANIAN V., HEYM B., BERGH S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLE S.T., PARKHILL J.,
SUBMITTED (FEB-1997) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-H37RV;
COLE S.T., PARKHIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-H37RV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
PUTATIVE TRANSMEMBRANE PROTEIN.
MTV037.14C.
MTV037.14C.
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLE S.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 96181548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-H37RV;
                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                                  823 AIHLHWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANSMEMBRANE.
SEQUENCE 967 AA;
                                                                                                                                                    Local Similarity 83.3% es 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 71.48 es 5; Conservative
                                                                                                         INLHWL
                                                                                                                                                                                                                                                                                                                                                                                                                       GINLHWL
.06C.
        7 (TREMBLREL. 03, C)
7 (TREMBLREL. 03, L)
7 (TREMBLREL. 03, L)
AL 41.3 KD PROTEIN.
                                                                                                                                                                                                198 AA;
                                                                                                            56
                                                                                                                                                                                                                                                                                                                    (TREMBLREL.)
(TREMBLREL.)
(TREMBLREL.)
GEPA, GEPB,
                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                        56
                                                                                                                                                                                                                                                                                                                                                                                                                                             829
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71.4%;
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            03, CREATED)
03, LAST SEQUENCE UPDATE)
03, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                 02, CREATED)
02, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
AND GEPC GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BARRELL B.G., RAJANDREAM M.A.; EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                  SCOTOBACTERIA; ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                 Score 50; DB 2; Len
Pred. No. 3.74e+01;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 53; DB 2; Ler
Pred. No. 1:15e+01;
2; Mismatches 0;
                                                                                                                                                                                                                             MCDONAGH M.B.,
                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93:3132-3137(1996).
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                                                                                                                                                                                            FA6F6C9D CRC32;
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                                                           372
                                                                                                                                                                                                                                                                                                                                                                         198
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BLOOM B.R., JA
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                                                                                                                                                                                                                              KATZ
                                                                                                                                                                     Length 198
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Е.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   967;
                                                                                                                                                                                                                            CHEETHAM B.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W.R.
                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                Gaps
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RESULT 6

ID Q21859;
AC Q21859;
AC Q21859;
DT 01-NOV-1996 (TREMBLREL. 01, CREATER OT 01-NOV-1996 (TREMBLREL. 01, LAST SE OT 01-AUG-1998 (TREMBLREL. 07, LAST AND DE ROPDI.3.

CE CAENORHABDITIS ELEGANS.
CC EUKARYOTA; METAZOA; ACOELOMATES; NE RN [1]

RP SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                            ACCOMENTATION OF THE PROPERTY 
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Best Local Similarity
Matches 4; Conser
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Best Local s
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01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEA11 OR BCEA.

MUS MUSCULUS (MOUSE).

EUKARYOTA; METAZOA; CHORDATA;

EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         PROC. NATL. ACAD. SCI. U.S.A. EMBL; U34272; G1098896; -. MGD; MGI:104983; CEA11. PFAM; PF00047; 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARCINOEMBRYONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAI M.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHEN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q60962;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROC. NATL ACAD. SCI. U.S.A. EMBL; Z83860; E290744; -. HYPOTHETICAL PROTEIN. SEQUENCE 372 AA; 41272 MW;
                                                                                                                                                                                                                                                                                                      323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 96181548.
PHILIPP W.J., POULET S.,
BALASUBRAMANIAN V., HEYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 GIQLHWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLE S.T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
COLE S.T., BARRELL B.
SUBMITTED (JAN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYCOBACTERIUM TUBERCULOSIS. PROKARYOTA; FIRMICUTES; ACT
                                                                                                                                                                                                                                                                 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. BROWN D., CHURCHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 GINLHWL
                                                                                                                                                                                                                                                               GINLHWL
                                                                                                                                                                                                                                                                                                  GVSIHWL 329
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Similarity 71.4%;
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASANAKA M.,
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                                                                                                                                                                                                                                                                                                                                       80.6%;
larity 57.1%;
Conservative
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01,
01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , RAJANDREAM M.A.;
EMBL/GENBANK/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                      WW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                 Score 50; DB 11; L
Pred. No. 3.74e+01;
3; Mismatches 0;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
(BRAIN CARCINOEMBRYONIC
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Pred. No. 3.74e+01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                          NEMATODA; SECERNENTEA; RHABDITIDA.
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BLOOM B.R.,
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                                                                                                                                                                                                                                                                                                                                                                        Length 386;
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RA WILSON R., ALMSCOUGH R., COPSEY T., COOPER J., COULSON A., CRAXTON M.,
RA BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRAXTON M.,
RA DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P.,
RA HAMKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J.,
RA KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
RA MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C.,
RA MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C.,
RA RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A.,
SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K.,
RA VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
RA WILKINSON-SPROAT J., WOHLDMAN P.;
RA WILKINSON-SPROAT J., WOHLDMAN P.;
DR EMBL; Z70035; E228187; -
DR EMBL; Z70035; E228187; -
DR SEQUENCE 435 AA; 50487 MW; C05D5854 CRC32;
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches
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005069;
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01-JUL-1997
01-JUL-1997
01-JUL-1997
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067845;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998 (TREMBLREL. 0
01-AUG-1998 (TREMBLREL. 0
01-AUG-1998 (TREMBLREL. 0
GLUTAMATE SYNTHASE SMALL
                                             TRANSPOSASE
                                                                                                                                                                                                                                                                                                                                                                                                                                       DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AE000770; G2984275; -.
SEQUENCE 476 AA; 52947 MW; 97B08285 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-VF5;
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    HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                   342 GVKIHWL 348
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                                                                (TREMBLREL.) (TREMBLREL.)
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                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                               (MUA)
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07,
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07, LAST ANNOTATION UPDATE)
SUBUNIT GLTD.
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Pred. No.
2; Misma
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Pred.
3; N
                                                                                        LAST
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                                                                                        SEQUENCE UPDATE)
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No: 3.74e+01
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AUJAY M., HUBE
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Matches
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Best Local Similarity
Matches 6; Conser
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                                                                                                                                                                                                             01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL 06, LAST SEQUENCE UPDATE)
TONB-DEPENDENT RECEPTOR HOMOLOG (FRAGMENT).
HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;
AEROBIC, MOTILE, HELICAL AND/OR VIBRIOID.
                                                                                                                                                                                                                                                                                                                      050198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.I., GLODEK A., KELLEY J.M., WEIDMAN J PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NUUYEN D.T., SADDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., SOGGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O., VENTER J.C.; SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M. MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCANNE J.D., SCOTT J.D., SHIKLEY R., LIU L.I., GLODEK A., KELLEY J.M., WEIDMAN PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R. HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O., VENTER J.C.; SCIENCE 269:496-512(1995).
                                                                                              MANOS J., KOLESNIKOW T., HAZELL S.L.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; AF015886; G2665532; -.
NON_TER 707 707
SEQUENCE 707 AA; 79095 MW; B82B1B54 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
WHITE O., CLAYTON R.A.,
SUBMITTED (SEP-1996) TO
EMBL; U32825; G1574318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
L TATUSOV R., MUSHEGIAN
BORODOVSKY M., RUDD K.E.
                                                                                                                                                                    STRAIN-RU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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          665
                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                           379 GIELHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 83.3%;
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               50
GINLAWL
                                                                                                                                                                                                                                                                                                                                                                                               GINLHW
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                                       Conservative
                                                      80.6%;
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., KOONIN E.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KERLAVAGE A.R., FLEISCHMANN R.D.; EMBL/GENBANK/DDBJ DATA BANKS.
                                       Score
Pred.
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                                         Mismatches
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No. 3.74e+01;
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No. 3.74e+01
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Matches
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SEQUENCE FROM N.A.

MEDLINE; 96203998.

LECOUTER J.E., WHYTE P.F.M., RUDNICKI M.A.;

ONCOGENE 12:1433-1440(1996).

-i- SUBCELLULAR LOCATION: NUCLEAR.

-i- SIMILARITY: BELONGS TO THE RETINOBLASTOMA
EMBL; U36799; G1045520; -.

EMBL; U50850; G1255232; -.
                                                                                                                                                                                                                                                                                                                                              J. BIOL.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
RETINOBLASTOMA-LIKE 2 (RETINOBLASTOMA-LIKE PROTEIN 2.
RBL2 OR P130) (RETINOBLASTOMA-RELATED PROTEIN P130)
(RETINOBLASTOMA-RELATED PROTEIN PRB2/P130) (RB-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q64700;
Q64700;
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01-JAN-1998
01-JUN-1998
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                                                                                                                                                                                                                         CELL GROWTH DIFFER.
                                                                                                                                                                                                                                                     GIORDANO A.;
                                                                                                                                                                                                                                                                    PERTILE P., BALDI A.,
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 96192345.
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE; 96199216.

CHEN G., GUY C.T., CHEN H.W., HU N., LEE

J. BIOL. CHEM. 271:9567-9572(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O25543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VENTER J.C.;
NATURE 388:539-547(1997).
EMBL; AE000597; G2314011;
TIGR; HP0876; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPD
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION U
IRON-REGULATED OUTER MEMBRANE PROTEIN (FRPB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUTHERIA; RODENTIA
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;
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LAST ANNOTATION UPDAT
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3.74e+01;
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Best Local :
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016084;
01-NOV-1996
01-NOV-1996
01-NOV-1996
SEQUENCE FROM N.A.

MEDLINE; 94074896.
HANNON G.J., DEMETRICK D., BE.
GENES DEV. 7:2378-2391(1993).
EMBL; S67171; G453132; -.
                                                                                                                                                                                        HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
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CONFLICT
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EMBL; D55627; D1025106; -.
SEQUENCE 1135 AA; 127816 MW; 369B2AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATTUS NORVEGICUS (
EUKARYOTA; METAZOA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U4
MGD; MGI
NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SPRAGUE-DAWLEY;
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les 5; Conser
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MGI:105085;
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N; CHORDATA;
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ENDO Y., UMEKI K.,
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Pred. No. 3.74e+01;
1; Mismatches 1
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local :
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Best Local Similarity 66.7%;
Matches 4; Conservative
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051122; PRELIMINARY; PRT; 322 AA.
051122;
01-NOV-1996 (TREMBLREL. 01; CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OT 14
PRELIMINARY; PRT; 1139 AA.
Q15073;
O1-NOV-1996 (TREMBLREL. 01, CREATED)
O1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
O1-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUB-PLACENTA /SPLEEN;
MEDLINE; 94074895.
LI Y., GRAHAM C., LACY S., DUNCAN A.M.V., WHYTE GENES DEV. 7:2366-2377(1993).
EMBL; X76061; G416031;
EMBL; X76061; G416031;
SEQUENCE 1139 AA; 128381 MW; 659C515E CRC32;
                                                                                                                                                                                           SEQUENCE FROM N.A.

ZHOU D., LEE F.F., APICELLA M.A.;
SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U35454; G1016752; -.

TRANSFERASE.
                                                                                                                                                                                                                                                                           NEISSERIA MENINGITIDIS.
PROKARYOTA; GRACILICUTES;
NEISSERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P130.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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50 GINLHWL 56
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50 GINLHWL 56
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nes 5; Conservative
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                                                                                                                                                                              322 AA;
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                                                                                                                                                                              36188 MW;
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                                                                                                                                                                                                                                                                                      SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                       Score 49; DB 2; Length 322; Pred. No. 5.49e+01; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 4; Length 1139; Pred. No. 3.74e+01; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB 4; Length 1139; Pred. No. 3.74e+01; 1; Mismatches 1; Indels
                                                                                                                                                                                8278FA9F CRC32;
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MPsrch_pp n on: protein - protein database search, using Smith-Waterman algorithm

abular output not generated. Tue Apr 20 14:08:59 1999; MasPar time 2.57 Seconds 56.748 Million cell updates/sec

Scoring table: Sequence: Description: Perfect Score: PAM 150 Gap 11 >US-08-836-455-1_1 (89-97) from trans.pep (3 of 3) 54 SDYSLTISS 9

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 11:part12
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 15.830; Variance 48.580; scale 0.326

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	BB	Ħ		Description	Pred. No.
ב	54	100.0	95	25	W18269		PrP 81 light chain va	1.90e+01
2	54	100.0	107	29	W44122		Light chain variable	1.90e+01
ω	54	100.0	107	25	W27121		e antib	1.90e+01
4	54	100.0	108	4	R21310		Light chain of M1f cl	1.90e+01
ۍ	54	100.0	108	4	R21286		Murine VL kappa group	1.90e+01
6	54	100.0	109	25	W18271	Ξ.	PrP 37 light chain va	1.90e+01
7	54		109	18	R52030		Light chain variable	1.90e+01
80	54	100.0	129	24	W22537		Murine anti-human cla	1.90e+01
9	54	100.0	145	25	W27119	-	Murine monoclonal ant	1.90e+01
10	54	100.0	146	4	P30251	<u>.</u>	Sequence of the leade	1.90e+01
11	54	100.0	243	18	W02280	÷	520C9 anti-c-erbB-2 t	1.90e+01
12	54		246	œ	R39569		Sequence of 520C9 sFv	1.90e+01
13	54	100.0	534	œ	R39571		Sequence of G-FIT.	1.90e+01
14	52	96.3	107	29	W44123		Light chain variable	3.15e+01
15	52	96.3	127	σ	R32125		Anti-IL2R alpha antib	3.15e+01
16	52	96.3	144	w	R15322		IL-2 chimeric antibod	3.15e+01
17	52	96.3	144	w	R15321	. .	IL-2 chimeric antibod	3.15e+01
18	51	94.4	107	14	R79247		Light chain variable	4.05e+01

5 50 92.	4 50 92.	3 50 92.	2 50 92.	1 50 92.	0 50 92.		8 50 92.	7 50 92.	6 50 92.	5 50 92.	4 50 92.	3 50 92.	2 50 92.	1 50 92.	0 50 92.	9 50 92.	8 50 92.	7 50 92.	6 50 92.	5 50 92.	4 50 92.	3 50 92.	2 50 92.	1 50 92.	0 51 94.	2 UL 34.
532 27 W35565	28	28 ¥	28 ¥	28 ¥	28 ¥	28 ¥	27 ¥	23 ¥	25 ¥	ω	ъ ъ	26 F	24 ¥	26 F	26 ¥	25 ¥	10 F	25 ¥	26 V	26 ¥	25 ¥	25 ¥	29 ¥	28 F	14 F	14
HindIII-Ecc	R. pipiens r	بر	R. pipiens r	₽. F	R. pi	R. pi	HindIII-EcoRl insert	Single chain a	Anti-c-erb	Vl-Lab		V1-Lab-Vh constructio	Mouse monoclonal ant	Light chain of	Light chain of full	Anti-Factor-IX	KM-60	Anti-Factor-		Humanised va	Anti-Factor-IX humani	Anti-Factor-IX hum	Mus musculus A717 an	Monoclonal antibod	Light chair	Light chain variab
٠	: .	:	: .	5.19e+01	: .	5.19e+01	: .	: .	: .	: .	: .	5.19e+01	: .	: .	: .	5.19e+01	:-	.15	. 15	.19	٠	•	•	•	•	4.000+01

ALIGNMENTS

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ample 9; Fig 8266-W18285 Libodies of	New antibodies to the s detection of infectious as RSE. C.TD or scrapie				WO9710505-A1. 20-MAR-1997.		Region	Region	•	Region	Region		Region	Region	-	Misc_difference		Region		Mus musculus.	Serstmann-Strassler-Scheinker Disease.	transmissible ne	central nervous	light chain vari	Prion protein; P	1998	W18269;	18269	
	to the infection	er	CALIFORNIA	U14840.		/note=	700Ce=	7588	/note=	/note= 4374	3642	/note-	2135	1020	/note-	ω	/note=	19	Locatio		m ence	urodeg	system	able r	n; Prp; heavy c	(first en	4000	pent i	
99pp; English. essent portions of the antibodies of the invention. The invention are able to bind the scrapie isoform of prion	to the scraple isoform of prion protein - used for ifectious prion proteins or for treating disease such	SB, Williamson RA;	А.			"framework region 4"	comprementarity determining region s		"framework region 3"	"complementarity determining region 2"		"framework region 2"		"complementarity determining region 1"	"unspecified amino acid"		"framework region 1"		Location/Qualifiers		bovine spongirorm encephatopatny; reitne spongirorm encephatopatny; Serstmann-Strassler-Scheinker Disease.		<pre>central nervous system spongiform encephalopathy; human; therapy;</pre>	-	Prion protein; Prp; heavy chain variable region; antibody; scrapie;		ò	de. QS AA	

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CC protein PrP-Sc in situ. Prions are infectious pathogens that cause CC central nervous system spongiform encephalopathies in humans and animals. The scrapie isoform of the prion protein (PrP-Sc) is necessary for both the transmission and pathogenesis of the transmissible neurodegenerative CC diseases of animals and humans. The antibodies can be used in a method of specifically bind to prion proteins associated with disease and do not CC bind to denatured PrP proteins not associated with disease. They can bind to the prion proteins of a specific species of mammals. They can also have CC the ability to neutralise infectious prions. The antibodies can be used for screening for the presence of prions in products such as CC neutralisation to purify products, for extraction of prion proteins or commentics. They can also be used for therapy, for diseases such as bovine spongiform encephalopathy, CC Serstmann-Strassler-Scheinker Disease, scraple or feline spongiform comentalismanthies.
                                                              Matches
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Best Local
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                                                                                                        therapy and immunodiagnosis
Example 1; Fig 2; 100pp; English.
The present sequence is the light chain variable region of the murine anti-human cancer antigen antibody (Ab) NR-LU-13.
A novel humanised Ab (hAb) binds the antigen bound by NR-LU-13. hAb specifically NRX451, or its conjugates can be used for the manufacture of a diagnostic or medicament for cancer diagnosis of treatment. The hAb has reduced immunogenicity and toxicity in humans, but retains the ability to bind the NR-LU-13 antigen.
Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                             (NEOR-) NEORX CORP
Graves SS, Henry A
                                                                                                                                                                                                                                                                                                                                                                                         11-DEC-1997.
06-JUN-1997; U10074.
07-JUN-1996; US-660362.
                                                                                                                                                                                                                                                                          Humanised antibody binds same human NR-LU-13 - useful for pre-targeting
                                                                                                                                                                                                                                                                                                                            Rees AR, Renojm, S. WPI; 98-042124/04.
                                                                                                                                                                                                                                                                                                                   N-PSDB; V02198
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9746589-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
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Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Light chain variable region of NR-LU-13 antibody.
Light chain; variable region; murine; mouse; human; cancer antigen; antibody; humanised; NR-LU-13; NRX451; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W44122 standard: Protein;
W44122;
05-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
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    89
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Sequence 95 AA;
                                                                            Local
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SDYSLTISS
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Similarity 100.0%;
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                                                          Conservative
 97
                             77
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89..97
/note=
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50..56
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--hes 0;
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RESULT
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CC Inis polypeptide sequence comprises a consensus sequence of murine CC light chain variable regions (VL) selected on the basis of identity CC light chain variable regions (VL) selected on the basis of identity CC light chain variable regions (VL) selected on the basis of identity CC light chain variable regions (VL) selected on the basis of identity CC light chain variable regions (VL) selected on the basis of identity CC light (NC) Sequences were obtained from a GenBank database capacity of the consensus (W27122) was also produced. 11D10 has at CC chain and 11 in the heavy chain). 8 Occur within CDRs and 10 CC cutside CDRs. 11D10 polypeptides and polynucleotides can be CC used in vaccines and pharmaceutical compositions for the treatment CC of human milk fat globule-associated diseases such as breast
                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
WO9201047-A.
23-JAN-1992.
                                                                                                                                                                                      Light chain of MIf clone, Fd; bacterionham
                                                                                                                                                                                                             R21310 standard; Protein; R21310; R21310; (first entry)
                                                                                                                                                         pilus; g3p;
specific bir
                                                                          region
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Chatterjee M, Chatter
WPI; 97-341690/31
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13-DEC-1996; US-575762.
20-DEC-1995; US-575762.
26-JAN-1996; US-591965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w27121 standard; Protein; 107
w27121;
04-JAN-1998 (first entry)
Murine antibody light chain v
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Murine antibody light chain variable region consensus.
Monoclonal antibody liD10; anti-idiotype antibody; mucin;
human milk fat globule; HMFG; tumour; breast cancer; vacc
                                                                                                                                                                                                                                                                                                                89 SDYSLTISS
                                                                                                                                        bacterlophage; gene III; filamentous; phagemid; capsid; coas; g3p; binding; adsorption; gene VIII; diverse repertoire; cific binding pairs; replicable genetic display package.
                                                                                                                                                                                                                                                                                                                                                                           9;
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                                                                                                                                                                                                                                                                                                                                                                        100.0%;
larity 100.0%;
Conservative
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                                          /label= CDR2
89..96
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                                                                                                                                                                                                                                                                                                                                                                 Score 54; DB 25; Le
Pred. No. 1.90e+01;
Wismatches 0;
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Pri display package.

Example 46; Fig 52; 109pp; English.

Comment specific for both hen and turkey egg lysozyme (HEL and TEL).

The sequence is the light chain of clone MIF encoding an scFv fragram ent specific for both hen and turkey egg lysozyme (HEL and TEL).

The DNA encoding the chain was amplified from a cDNA library prepd.

Comment specific for both hen and turkey egg lysozyme (HEL and TEL).

The DNA encoding the chain was amplified from a cDNA library prepd.

Compare the spleen of an unimmunised mouse. The corresponding heavy chain was also amplified from an existing construct, pSW1-VHD1.3

Compare an scFv construct which was ligated into the fdCAT2

Covector for expression on the surface of fd bacteriophage. In this way, the VL domain was replaced by a library of VL domains to allow for selection of a broader range of antibody specificities. Several colones were isolated which bound to TEL (the parent antibody D1.3 colones were isolated which bound to TEL (the parent antibody D1.3 colones were isolated which bound to TEL (the parent antibody D1.3 colones were isolated which bound to TEL (the parent antibody D1.3 colones were clones, MF1 and M21 are given in R21310 and R21311

Compared these clones, MF1 and M21 are given in R21310 and R21311

Compared the sequences of the light chains of two of these clones, MF1 and M21 are given in R21310 and R21311

Compared the sequences of the light chains of the light chain is given in R21309.
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Matches
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McCafferty J, Pope AR, Johnson K,
Jackson RH, Holliger KP, Marks JJ
Winter GP, Bonnert TP;
WPI: 92-056882/07.

Producing members of specific bin
recombinant host cells with a see
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10-JUL-1990; GB-015198.

19-OCT-1990; GB-022845.

12-NOV-1990; GB-024503.

06-MAR-1991; GB-004744.

15-MAY-1991; GB-010549.

(CAMB-) CAMBRIDGE ANTIBODY.
W09201047-A.
23-JAN-1992; G01134.
10-JUL-1991; GB-015198.
10-JUL-1990; GB-022845.
12-NOV-1990; GB-022845.
12-NOV-1990; GB-024704.
15-MAY-1991; GB-004744.
15-MAY-1991; GB-010549.
(CAMB-) CAMBRIDGE ANTIBODY.
(MEDI-) MED RES COUNCIL.
MCCafferty J, Pope AR, Johnson K:
Jackson RH, Holliger KP, Marks JI
Winter GP, Bonnert TP;
Whiter GP, Bonnert TP;
WPI; 92-056862/07.
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R21286 standard; Protein; 108
R21286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine VI kappa group V chain "a", specific for phOx.

Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus; g3p; binding; adsorption; gene VIII; diverse repertoire; specific binding pairs; replicable genetic display package.
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Similarity 100.0%;
9; Conservative
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89..96
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50..56
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= CDR3
/note=" D-X-G-X-X motif "
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                                                                        Hoogenboom HRJ, Griffiths Clackson TP, Chiswell DJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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Example 21; Fig 24; 209pp; English.

Example 21; Fig 24; 209pp; English.

The VK sequence is one of seven (R21286-92) found to be expressed from a single chain Fv library from an immunised mouse. The library produces a diverse repertoire of antibody fragments specific for a produce a diverse repertoire of antibody fragments.
W09710505-A1.

20-MAR-1997.

13-SEP-1996; U14840.

14-SEP-1995; US-528104.

(REGC ) UNIV CALIFORNIA.

Burton DR, prusiner SB, Williamson RA;

WRI; 97-202357/18.

New antibodies to the scrapie isoform of prion protein New Author of infectious prion proteins or for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9-JAN-1998 (first entry)

PrP 37 light chain variable region.

PrP 37 light chain variable region.

Prion protein; Prp; heavy chain variable region; antibody; scraple;

Prion protein; Prp; heavy chain variable region; FrP-Sc; pathogen; fatal familial insomnia;

light chain variable region; PrP-Sc; pathogen; fatal familial insomnia;

central nervous system spongiform encephalopathy; human; therapy;

transmissible neurodegenerative disease; Creutzfeldt-Jakob Disease;

bovine spongiform encephalopathy; feline spongiform encephalopathy;

Serstmann Strassler-Scheinker Disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W18271
W18271;
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See also R21260-307,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AA;
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/note=
57..88
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89..97
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35..49
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24..34
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98..109
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Pred. No. 1.90e+01
0; Mismatches
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            such
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as BSE, CJD or scrapie Example 9; Fig 6; 99pp; W18266-W18285 represent

English

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RESULT
ID RESULT
AC R5
ET r6
ET r6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC willife-willing represent portions of the antibodies of the invention. The CC antibodies of the invention are able to bind the scrapic isoform of prion CC central nervous system sponsitions are infectious pathogens that cause CC The scrapic isoform of the prion protein [Prior CC diseases of animals and humans. The antibodies can be used in a method of diseases of animals and humans. The antibodies can be used in a method of CC specifically bind to prion proteins associated with disease and do not to denatured prior proteins not associated with disease and do not to prion proteins of a specific specific with disease. They can bind to denatured prior proteins not associated with disease and do not the ability to neutralise infectious prions. The antibodies can be used for screening for the presence of prions in products such as prior therapy, for diseases such as bovine sponsiform encephalopathy, serstmann-Strassler-Scheinker Disease, scrapie or feline sponsiform encephalopathy, serstmann-Strassler-Scheinker Disease, scrapie or feline sponsiform
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Best Local S
Matches
                                                                                                                                                             13-APR-1994.
07-SEP-1993; 307051.
09-SEP-1992; US-942245.
(PEDE/) PEDERSSEN T.
WPI; 94-12030/15.

Method of resurfacing of rodent antibodies to produce humanised antibody forms - for producing non-human antibodies with improved therapeutic efficiency by presenting human surface on V-region Example 1; Fig 3A; 230pp; English.

The present sequence is that of the light chain variable (LC VR) of murine antibody glb2. This sequence was aligned with 11 other lantibody LC VRs and a set of framework positions of surface expose
                                                                                                                                         (IMMU-) IN
Guild BC,
                                                                                                                                                                                                                                EP-592106-A1.
                                                                                                                                                                                                                                                                                                                                                                           region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modelling;
Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain variable region of murine antibody glb2.
antibody; humanised; murine; human; heavy chain; light; variable; framework region; complementarity determining region; reshaping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R52030 standard; Protein; 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-1996
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                                                                                                                                   IMMUNOGEN INC.
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                           /label= FR_3
89..97
/label= CDR_3
98..109
/label= FR_4
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35..49
                                                                                                                                                                                                                                                                                                                        /label- CDR_2
57..88
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24..34
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50..56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  residue; modify.
                                                                                                                                                                                                                                                                                                                                                                                            "CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                          "FR 1"
                                                                                                                                                                                                                                         FR_4
                                                                                                                                                                                                                                                                       CDR_3
                                                                                                                                    Rees
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                                                                                                                                   AR,
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Pred. No. 1.90e+01;
0; Mismatches (
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                      other known
      exposed
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RESULT
ID W2
AC W2
DT 04
DE MU
KW MC
KW hu

W27119

standard;

Protein; 145

W27119;
04-JAN-1998 (first entry)
04-JAN-1998 (first entry)
Murine monoclonal anti-idiotype antibody 11D10 VL region.
Monoclonal antibody 11D10; anti-idiotype antibody; mucin;
human milk fat globule; HMFG; tumour; breast cancer; vacc

Ş 밁

68 91

sdysltiss

99

0;

Indels

0

Gaps

0;

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RESULT ACCORDING TO ACCORD ACC
                                                                                                                                                                                                               PT Recombinant conjugate antibody mol., modified for delivering an prantigen - elicits enhanced immune response without the use of adjuvant to generate antibodies which are useful in vaccines or prantigen recombinant conjugate antibody molecules comprise a monoclonal condition of a surface structure of antigen presenting control of a surface structure of antigen presenting conclusively at one or more preselected sites. The conjugate is capable contains at least one antigen confident to accomply at one conjugates are useful as vaccines and are able to elicit an enhanced immune response without the use of an adjuvant. Consider anti-numan class I monoclonal antibody secreted by hybridoma conditions and specific example, a conjugate was constructed using the murine consists of a tandemly linked T and B cell epitope derived from HIV MN strain. Consists of from 44H104 which was used in the preparation of a conjugate with
                      Query Match
Best Local s
Matches
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                                                                                                                                                                                         antigen CLTB36.
Sequence 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CONN-) CONNAUGHT LAB LTD.
Anand NN, Barber BH, Cat
WPI; 97-077271/07.
N-PSDB; T77851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-NOV-1997 (first entry)
Murine anti-human class II monoclonal antibody 44H104 VL chain.
Antibody: light chain; variable region; hybridoma cell line 44H
immune response; enhance; stimulate; vaccine; immunodiagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid residues was determined. This information can be used in a method to determine how to modify a rodent antibody or fragment by resurfacing in order to produce a humanised rodent antibody. Residues (determined from alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 63, 66, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 86, 73, 
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07-JUN-1995; US-483576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus. W09640941-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen delivery.
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W22537 standard; Protein; 129
W22537;
             69 sdysltiss
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                                                    000
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Score 54; DB 24;
Pred. No. 1.90e+01;
0; Mismatches 0
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Pred. No. 1.90e+01;
0; Mismatches 0
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                                                                           Length 129;
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                                                                                                                                        В
                                                                                                                                                                                                                                  This polypeptide sequence comprises the light chain variable region (VL) of monoclonal anti-idiotype antibody lillio produced by hybridoma cell line ATCC 12020. Illio was obtained by immunising the hybridoma cell line ATCC 12020. Illio was obtained by immunising contained mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype cresponse. It elicits an immune response against a specific epitope of a high mol.wt. mucin of human milk fat globule (HMFG). It induces an immunological response to HMFG in mice, rabbits, monkeys and patients with advanced HMFG-associated tumours. Pharmaceutical compositions and vaccines comprising Illio, lillio polypucleotides (see also T85149-50) are claimed.

CC and/or lillio polypucleotides (see also T85149-50) are claimed.

CC Also claimed are diagnostic kits and methods of using 11D10, 11D10 polypeptides and/or lillio polypucleotides, including methods of treating HMFG-associated tumours. Illio is also used in a claimed content of palliating HMFG-associated disease and in claimed kits to detect or quantify anti-HMFG antibody.
                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Consei
 P30251 standard; peptide; 146 A
P30251;
P30251;
25-MAY-1992 (first entry)
Sequence of the leader, variabl
the constant region of the kapp
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20-DEC-1995;
26-JAN-1996;
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Chatterjee M, Chatterjee
WPI; 97-341690/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                              especially breast cancer
Claim 9; Page 94; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monoclonal anti-idiotype antibody 11D10 - elicits against human milk fat globule disease associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T85149.
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larity 100.0%;
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/note= "complementarity determining
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117
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variable region and first 16 AAs of
the kappa-chain (light chain) of MOPC41.
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                                                                                                                                                                 re 54; DB 25; Le
1. No. 1.90e+01;
Mismatches 0;
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Matches
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N-PSDB; 736880.

Compsns. contg. antigen-targetting antibody fragment const comprising dimer of single-chain Fv fragments
Example 1; Columns 33-36; 30pp; English.

Variable heavy (VH) and variable light (VL) genes were clo
a 520C9 hybridoma cDNA library, using probes directed towa
antibody constant and joining regions. A two single chain
gene was constructed by connecting the VH and VL genes wit
Ser rich polypeptide linker. The resulting 520C9 two sFv g
which encodes the present sequence, was inserted into an e
                                                                                                                                                                                                                                                                                                                                              09-JUL-1996.
06-FEB-1992;
06-FEB-1992;
07-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT 1996 (first entry)
29-OCT 1996 (first entry)
520C9 anti-c-erbB-2 two single chain Fv construct.
520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sFv construct; polypeptide linker; C-terminal amino acid sequence; In vivo imaging; drug targetting experiment; homodimer; increased; binding avidity; tissue retention time.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region
                                                                                                                                                                                                                                                 (CHIR ) CHIRON CORP.
(CREA.) CREATIVE BIOMOLECULES INC.
HOUSTON LL, HUSTON JS, Oppermann
WPI; 96-333194/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-1982;
05-DEC-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosis; therapy; immunoglobulin. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                            US5534254-A.
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(DNAX-) DNAX RES INST.
MOORE KW, Zaffaroni A;
WPI; 83-772290/39.
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Similarity 100.0%;
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US-358414.
US-558551.
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US-133804.
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23..130
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131..146
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                                                                                                                                                                                                                                                                                                                                         I antigen for imaging or treating breast or ovarian cancer etc.

Claim 4; pages 60-61; 87pp; English.

C c-erbB-2 refers to a protein antigen expressed on the surface of the control of about 5.3 (see 046083, R39568). A single chain Fv (sFv) of about 5.3 (see 046083, R39568). A single chain Fv (sFv) is a covalently linked VH-VL heterodimer which is expressed from a gene fusion including VH- and VL- encoding genes connected by a peptide-encoding linker. Such linker sequences are set forth in AA residues 116-135 in R39569, which includes part of the 16 AA linker sequences in R39572. Using 046084 for the 520C9 monoclonal antibody, a single chain polypeptide can be produced having a binding affinity for a c-erbB-2 related antigen. 'X' in R39569 are fers to the location of a stop codon in 046084.
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Synthetic.
W0316185-A.
19-AUG-1993.
05-FEB-1993; U01055.
06-FEB-1992; US-831967.
                                                                                              ULT 13
R39571 standard; P
R39571;
07-FEB-1994 (firs
Sequence of G-FIT.
                                                                               Tumour antigen; c-erbB-2; G-FIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-FEB-1993; U01055.
06-FEB-1992; US-831967.
(CETU ) CETUS ONCOLOGY CORP.
(CREA-) CREATIVE BIOMOLECULES INC.
HOUSTON LL, HUSTON JS, Oppermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of 520C9 sFv protein.
Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; biosynthetic single polypeptide chain binding site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; Q46084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R39569 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vector, transformed into E. coli, and protein expression induced by the addn. of IPTG to the culture medium.

A compsn. comprising a carrier and the 2 sFv protein prod. can be used for in vivo imaging, and drug targetting experiments. The 2 sFv protein prod. is a homodimer, in which both fragments target the same antigen, therefore giving greater binding avidity and longer tissue retention times, compared to individual sFv protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New single chain Fv polypeptide binding
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                                                                                                                                                                                                             SDYSLTISS
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                                                                                                                                             standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fragments.
                                                                                                                                                                                                                                                                         h 100.0% Similarity 100.0% 9; Conservative
                                                                                                                                                                                                                                                                                                                                       246 AA;
                                                                                                           (first entry)
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Pred. No. 1.90e+01;
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No. 1.90e+01;
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Matches
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Best Local :
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WPI; 98-042124/04.
Humanised antibody binds same human cancer antigen as antibon NR-LU-13 - useful for pre-targeting methods, conventional at therapy and immunodiagnosis Example 1; Fig 3; 100pp; English.
The present sequence is the light chain variable region of humanised murine anti-human cancer antigen antibody (Ab) NR
                                                                                                                                                                                                hAb, specifically NRX451, or its conjugates can be used for the manufacture of a diagnostic or medicament for cancer diagnosis treatment. The hAb has reduced immunogenicity and toxicity in humans, but retains the ability to bind the NR-LU-13 antigen.
                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                              A novel humanised Ab (hAb) binds the antigen bound by NR-LU-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1996; US-660362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-1997.
06-JUN-1997; U10074.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Light chain variable region of humanised NR-LU-13 antibody Light chain; variable region; murine; mouse; human; cancer antibody; humanised; NR-LU-13; NRX451; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New single chain Fv polypeptide binding to C-erbB-2 tumour antigen for imaging or treating breast or ovarian cancer etc. Example: pages 65-68; 87pp; English. C-erbB-2 refers to a protein antigen expressed on the surface of tumour cells. such as breast and ovarian tumour cells, which is an approx. 200,000 mol. wt. acidic glycoprotein having an isolelectric pt. of about 5.3 (see Q46083, R39568).
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(CREA-) CREATIVE BIOMOLECULES INC.
Houston LL, Huston JS, Oppermann
WPI; 93-272889/34.
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RESULT 15 ID R32125 standard;

Protein;

127

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PF 30-DEC-1991; 143214.

PF 30-DEC-1991; DE-143214.

PR 30-DEC-1991; DE-143214.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

KALUZA B, Riethmueller G, Scheuer W, Weidle U;

WAT; 93-037582/05.

PN N-SDB; Q36611.

PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R beta antibodies

PT comprises monoclonal anti-D4 antibodies and monoclonal anti-IL2R beta antibodies

PS (laim 6; Page 13; 18pp; German.

CC This sequence is the light chain variable region of a preferred

CC anti-IL2R alpha monoclonal antibody for use in the claimed

CS (SCACC 90071905). The anti-IL2R alpha antibody is used with at least

CC one anti-CD4 antibody. Individually the antibodies are strongly

CC (ECACC 90071905). The anti-IL2R alpha antibodies are strongly

CC (ECACC 90071905) and when used together their immunosuppressive properties

CC are improved; they synergistically inhibit T-helper cell

CC proliferation to effectively inhibit transplant rejection at low

CC doses without significantly reducing the general immune response.

CC See Q36607-Q36616.
                                                                                                                                                               Query Match 96.3%;
Best Local Similarity 88.9%;
Matches 8; Conservative
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Anti-IL2R alpha antibody 179 light chain variable region.
immunosuppression; tissue transplantation; graft; L chain; V region;
T-helper cell inhibition; transplant rejection; MAD;
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02-JUN-1993
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116..127
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arch completed: Tue Apr 20 14:09:12 1999 b time : 13 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm m on: Tue Apr 20 13:57:31 1999; MasPar time 2.58 Seconds

Tabular output not generated.

Description:
Perfect Score:
Sequence: >US-08-836-455-2 (50-66) from US08836455.pep (2 of 3) 131

1 GINLHWLQQEPDGTIKR 17

Scoring table: PAM 150 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swissprot

Statistics: Mean 28.762; Variance 43.396; scale 0.663

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

esult Query No. Score Match L	110 84.	υı	76 58.	76 58.	76	76 58.	76 58.	70 53.	67 51.	67	67 51.	66	66 50.	- 66 50.	65 49.	64 48.	64 48.		63 48.	63 48.	63 48. 48.	53 448. 48.	
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Pred. No.	1.23e-09	4.59e-03	1.10e-02	1.10e-02	1.10e-02	1.10e-02	1.10e-02	1.38e-01	,	. /ue-	4.70e-01	4.70e-01 4.70e-01 4.70e-01	.70e .70e .70e	4.70e-01 4.70e-01 4.70e-01 7.02e-01 7.02e-01	4.70e-01 4.70e-01 4.70e-01 7.02e-01 7.02e-01 7.02e-01	4.70e-01 4.70e-01 7.02e-01 7.02e-01 7.02e-01 7.02e-01 1.04e+00	4.70e-01 4.70e-01 4.70e-01 7.02e-01 7.02e-01 7.02e-01 7.02e-01 1.04e+00 1.55e+00	4.70e-01 4.70e-01 7.02e-01 7.02e-01 7.02e-01 7.02e-01 1.02e-01 1.55e+00 1.55e+00	4.70e-01 4.70e-01 4.70e-01 7.02e-01 7.02e-01 7.02e-01 1.02e+00 1.55e+00 2.28e+00	4.70e-01 4.70e-01 4.70e-01 7.02e-01 7.02e-01 7.02e-01 1.04e+00 1.55e+00 2.28e+00	4.70e-01 4.70e-01 7.02e-01 7.02e-01 7.02e-01 1.04e+00 1.55e+00 2.28e+00 2.28e+00	4.70e-01 4.70e-01 4.70e-01 7.02e-01 7.02e-01 7.02e-01 7.02e-01 1.54e+00 1.55e+00 2.28e+00 2.28e+00 2.28e+00	4.70e-01 4.70e-01 7.02e-01 7.02e-01 7.02e-01 7.02e-01 1.04e+00 1.55e+00 2.28e+00 2.28e+00 2.28e+00 3.35e+00

Query Match 84.0%; Score 110; DB 1; Length 130; Best Local Similarity 82.4%; Pred. No. 1.23e-09;

45	44	43	42	41	40	39	38	37	36	ω 5	34	ω ω	32	31	30	29	28	27	26	25	*
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44.3	44.3	44.3	44.3	44.3	45.0	45.0	45.0	45.0	45.0	45.0	45.0	45.0	45.0	45.0	45.0	45.0	46.6	46.6	46.6	46.6	
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YLJ6_CAEEL	HEMA_IAHLO	HEMA_IAHSP	HEMA_IAHSW	GSHE_RAT	EPA4_MOUSE	EPA4_CHICK	EPA4_HUMAN	HEMA_IAHCD	HEMA_IAHDE	HEMA_IAHNN	Y4NM_RHISN	WCAL_SALTY	HV3U_HUMAN	Y128_SYNP6	KV3E_MOUSE	CYPC_STRHA	YCAI_ECOLI	HEMA_IACKV	HEMA_IASTA	YBES_ECOLI	DATE TO COLL
HYPOTHETICAL 272.0 KD	HEMAGGLUTININ PRECURSO	HEMAGGLUTININ PRECURSO	HEMAGGLUTININ PRECURSO	EPIDIDYMAL SECRETORY G	EPHRIN TYPE-A RECEPTOR	EPHRIN TYPE-A RECEPTOR	EPHRIN TYPE-A RECEPTOR	HEMAGGLUTININ PRECURSO	HEMAGGLUTININ PRECURSO	HEMAGGLUTININ PRECURSO	HYPOTHETICAL 57.3 KD P	PUTATIVE COLANIC ACID	IG HEAVY CHAIN V-III R	HYPOTHETICAL 12.8 KD P	IG KAPPA CHAIN V-III R	PUTATIVE POLYKETIDE CY	HYPOTHETICAL 87.3 KD P	HEMAGGLUTININ PRECURSO	HEMAGGLUTININ PRECURSO	HYPOTHETICAL 55.3 KD P	OME PROTEIN.
1.49e+01	1.49e+01	1.49e+01	1.49e+01	1.49e+01	1.03e+01	1.03e+01	1.03e+01	1.03e+01	1.03e+01	1.03e+01	4.90e+00	4.90e+00	4.90e+00	4.90e+00	4.300						

ALIGNMENTS

RESULT ID AC PO

KV5J_MOUSE

P01643;

δÃ 밁

50 52 Matches

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SEQUENCE.
STEAIN-A/J;
MEDLINE, 82150934.
SIEGELMAN M., CAPRA J.D.;
PROC. NATL. ACAD. SCI. U.S.A.
-!- ANTI-ARSONATE HYBRIDOMA PI
PIR; A01927; KVMSAR.
HSSP; P01607; 1FAI.
                                                                                                                                                                                                                                                                                           P01646;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-V REGION (HP 123E6).
MUS MUSCULUS (MOUSE).
EUKARYCTA; METAZOA; CHORDATA; VERTEBRATA; TET
                                                                                                                                IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-CCT-1993 (REL. 27, LAST ANNOTATION UPDAT
IG KAPPA CHAIN V-V REGION (MOPC 173).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I- THIS CHAIN WAS ISOLATED IR; A01926; KVMS73.
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THIS CHAIN WAS ISOLATED FROM
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                                                                                                                         ANTIARSONATE ANTIBODY.
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COMPLEMENTARITY-DETERMINING
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COMPLEMENTARITY-DETERMINING
                                                                                          COMPLEMENTARITY-DETERMINING
                                                                                                             FRAMEWORK
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COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
BY SIMILARITY.
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Best Local
PROC: MITARSONAL PIR; A01927; KVMSAR.
PIR; A01927; KVMSAR.
HSSD; P01607; 1FAI.
HSSD; P01607; 1FAI.
23
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Best Local s
Matches
                                                          KV5L_MOUSE STANDARD;
PO1645;
21-JUL-1986 (REL. 01, CREAT
21-JUL-1986 (REL. 01, LAST
01-OCT-1993 (REL. 27, LAST
IG KADPA CHAIN V-V REGION (
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DISULFID
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                                                                                                                                              SEQUENCE
                                                                                                                                                                            EUTHERIA;
                                                                                                                                                                                             EUKARYOTA;
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NATURE 304:320-324(1983).
'I- ANTI-2-PHENYL OXAZOLONE (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P04946;
13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UP
01-OCT-1993 (REL. 27, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                             33 LNWYQQKPDGTVK
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                                                                                                                                                                                                                                                                                                                                                               LHWLQQEPDGTIK
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METAZOA;
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27, LAST ANNOTATION UPDAT
V REGION (HP 93G7)
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69.2%;
    ANTIARSONATE ANTIBODY FRAMEWORK 1.
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Pred. No. 1.10e-02;
2; Mismatches
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
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Pred. No. 1.10e-02;
                                                                           78:7679-7683(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 108,
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Matches Best Query Match

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DISULFID
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SEQUENCE
                                                                              KV5N_MOUSE STANDARD; PRT; 108 AA. P01647; P1647; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE) IG KAPPA, CHAIN V-V REGION (HP 124E1).

MUS MUSCULUS (MOUSE).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETEUKARYOTA; METAZOA;
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DOMAIN
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21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
10-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
10 KAPPA CHAIN VVC REGION (HP R16.7).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
SEQUENCE.
STRAIN-A/J;
MEDLINE; 82150934
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HSSP; P01607; 1FAI.
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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PROC. NATL. ACAD.
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MEDLINE; 82150934
                                                                      EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUTHERIA; RODENTIA.
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nes 9; Conser
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                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                      RODENTIA.
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FRAMEWORK 1.
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BY SIMILARITY.
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BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
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                                                                                       VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78:7679-7683(1981).
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No. 1.10e-02;
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, 1.10e-02;
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P01648;
21-JUL-1986 (REL. (
21-JUL-1986 (REL. (
01-OCT-1993 (REL. )
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PROC. NATL. ACAD. SCI. U.S.A
-1- ANTI-ARSONATE HYBRIDOMA
PIR; A01927; KVMSAR.
                                                                                                                                                                                                                                                                       DOMAIN
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HSSP; P01607; 1FAI.
IMMUNOGLOBULIN V REG!
                                                                                                                                                                                                                                                                                                                                                                             PROC. NATL. ACAD. SCI. U.S.
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MEDLINE; 82150934.
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EUKARYOTA; METAZOA;
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P01607; 1FAI.
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                                                                                                                                                                                                                                                                                                                         REGION;
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01, LAST SEQUENCE UP
27, LAST ANNOTATION
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DMA PROTEIN.
                                                                                                                                                                                                                                                                                                                         ANTIARSONATE ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                               S.A. 78:7679-7683(1981).
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Pred. No.
3; Misma
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Pred. No.
2; Misma
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BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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YCAJ_ECOLI STAN P45526; P75833; 01-NOV-1995 (REL. 3 01-NOV-1997 (REL. 3 01-NOV-1997 (REL. 3 NYPOTHETICAL 49.6 K

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, LAST EQUUENCE UPDATE;
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PROTEIN IN LOLA-SERS INTERGENIC REGION.

STANDARD;

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Best Local Similarity
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P26094;
01-MAY-1992
01-MAY-1992
01-FEB-1995
                      -i- FUNCTION: HEMAGGLUTIN, IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-i- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMER IS FORMED BY TWO CHAINS (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
EMBL; X62553; G59190; -
PIR; S22013; S22013.
HSSP; P03437; 1HGD.
                    ENVELOPE
                                                                                       GIBSON C.A., DANIELS R.S., VIRUS RES. 22:93-106(1992)
                                                                                                          SEQUENCE FROM N.A. MEDLINE; 92230399.
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                                                                                                                                             UNFLUENZA
                                                                                                                                                               REMAGGLUTININ
                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL PROTEIN; ATP-BINDING.
NP_BIND 57 64 ATP /
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HAERTLEIN M., MADI
NUCLEIC ACIDS RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
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EMBO J. 14:3365-3372(1995).
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MEDLINE; 95354654.
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STRAIN-K12 / MG1655;
BLATTNER F.R., PLUNKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION.
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ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 367-447
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                PROTEIN; HEMAGGLUTININ;
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                                                                                                                                   VIRUS (STRAIN
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(REL. 22, LAST SEQ
(REL. 31, LAST ANN
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RES. 15:1005-1017(1987).
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EMBL/GENBANK/DDBJ
                                                                                                                              A/EQUINE/CAMBRIDGE/1/63).
VIRUSES; NEGATIVE-STRAND; ORTHOMYXOVIRIDAE.
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                                                                                              OXFORD J.S.,
                                                                                                                                                                   SEQUENCE UPDATE)
ANNOTATION UPDATE)
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Pred. No.
5; Misma
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HA1 CHAIN
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0E65785D CRC32;
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              GLYCOPROTEIN;
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4.70e-01;
                                                                                            MCCAULEY J.W.;
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                                                                                                                                                                                                                                                                                           Length 447;
             SIGNAL
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TA BANKS.
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Best Local s
Matches
                                                                                                                                  UFO2_MANES STANDARD; PRT; 346 AA Q40285; Q1-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE PLAYONOL 3-O-GLUCOSYLTRANSFERASE 2 (EC 2.4.
MANIHOT ESCULENTA (CASSAVA) (MANIOC)
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGI
EUPHORBIALES; EUPHORBIACEAE.
[1]
                                                                                      FLAVONOID 3-O-GLUCOSYLTRANSFERASE GT2 OR UGT73A2.
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SEQUENCE
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (REL.
01-MAY-1992 (REL.
01-FEB-1995 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMA_IAHPR
P26101;
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                                                                                                                                                                                                                                                                                                                                                                          51 INLHWLQQEPDGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFLUENZA A VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Conservative
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ENVELOPED VIRUSES; NEGATIVE-STRAND; ORTHOMYXOVIRIDAE
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22, LAST SEQUENCE UP
31, LAST ANNOTATION
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Pred. No.
5; Misma
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Pred. No. 4.70e-01
5; Mismatches
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                            ANGIOSPERMAE; DICOTYLEDONEAE;
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d. No. 4.70e-01;
Mismatches 3;
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                                                                                                             EC 2.4.1.91)
(FRAGMENT).
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                                                                                                                                                                                                                                                                  346 AA.
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                                                                                                                                     (UDP-GLUCOSE
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Best Local
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DNA SEC. 5:41-49(1994).

-i- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS,

GLYCOSYLATION REACTION ALLOWS THE ACCUMULATION OF ANTHOCYAN

PIGMENTS (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: UDD-GLUCOSE + A FLAVONOL - UDD + FLAVON

3-O-D-GLUCOSIDE.

-i- PATHWAY: ONE OF THE ESSENTIAL AND TERMINAL STEPS IN THE
                                                                                  CONFLICT
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 92142506
SELIGER L.S., GIANTINI M., SHATKIN A.J.;
VIROLOGY 187:202-210(1992)
-I- FUNCTION: THE VIRAL OUTER SHELL POLYPEPTIDES, OF WHICH SIGMA-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X77461, G453255; -...
PROSITE; PS00375; UDPGT; 1.
TRANSFERASE; GLYCOSYLTRANSFERASE; MULTIGENE FAMILY
                                                                                                                       EMBL; M13139; G333720; -
EMBL; X61586; G61948; -.
PIR; A24245; MNXRS4.
PIR; A42192; A42192.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 86215171. ATWATER J.A., MANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A TISSUE-COTYLEDON;
                                                                                                            COAT PROTEIN
                                                                                                                                                                                                                                                                                                                                    BIOCHEM. BIOPHYS. RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                           /IRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                        REOVIRUS (TYPE 1 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 MQWLDDQPEGSV 147 ::||:::|::
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129 VELNWLQVDPNSMFR 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTHOCYANIN BIOSYNTHETIC PATHWAY.

TISSUE SPECIFICITY: EXPRESSED IN COTYLEDONS, ROOTS AND LEAVES.

DEVELOPMENTAL STAGE: MAXIMUM EXPRESSION IN COTYLEDONS THAT JUST

EMERGED FROM THE SEED COAT. LOW LEVELS IN HYPOCOTYLS AND

INCREASING LEVELS IN ROOTS THROUGHOUT THIS PERIOD OF DEVELOPMENT.

SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
                                                                                                                                                                                           ONE, IMPOSE STRUCTURAL CONSTRAINTS THAT PREVENT ELONGATION OF NASCENT TRANSCRIPTS BY THE VIRION-ASCED RNA-POLYMERASE. SIGMA-3 ALSO IMHEBIS HOSE PROTEIN SYNTHESIS IN INFECTED MOUSE LELLS AND MAY BE INVOLVED IN SWITCHING FROM CELLULAR TO VIRAL MRN
                                                                                                                                                                              CELLS AND MAY BE INVOLVED IN SWITCHING FRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHWLQQEPDGTI
                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.
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                                                                                  365 AA;
                                                                                               325
                           Conservative
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                                                                                                                                                                                                                                                                                                                                    MANEMITSU S.M., SAMUEL C.E.;
HYS. RES. COMMUN. 136:183-192(1986).
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                                        50.4%;
                                                                                41156 MW;
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Pred.
                                        Score 66; DB 1;
Pred. No. 7.02e-
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B001989A CRC32;
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                         SEQUENCE FROM N.A.
MEDLINE; 80054765.
PORTER A.G., BARBER C., CA
EMTAGE J.S.;
NATURE 282:471-477(1979).
                                                                                                                       21-JUL-1986
21-JUL-1986
01-FEB-1995
                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
CARBOHYD
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01-APR-1990
01-NOV-1995
                                                                                                                                                  HEMA_IAFPR
P03459;
                                                                                                                                                                                                                                                                                                                                                             SIGNAL
CHAIN
CHAIN
                                                                                                                                                                                                                                                                                     CONFLICT
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-!- FUNCTION: HEMAGGLUTININ IN SERSONISIBLE FOR ATTACHING THE VIRUS CELL RECEPYORS AND FOR INITIATING INFECTION.
-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMER IS FORMED BY TWO CHAIN (HAI AND HA2) LINKED BY A DISULFIDE BOND.
EMBL; M31689; G323975; -.
EMBL; J02164; G324163; -.
EMBL; J02169; A04069.
PIR; A04069; A04069.
HSSP; P03437; 1HGD.
                    NATURE [2]
                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                           ENVELOPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-108 FROM N.A. MEDLINE; 82150925.
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ORLICH M., KHATCHIKIAN D.,
VIROLOGY 176:531-538(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEMAGGLUTININ PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEMA_IATKR P03458;
MUTANTS TS1 AND TS227 MEDLINE; 87080266.
                                                                                   VIRIDAE;
                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                               HEMAGGLUTININ
                                                                                  INFLUENZA A VIRUS (STRAIN
VIRIDAE; SS-RNA ENVELOPED
                                                                                                                                                                                                                    239 IDFHWLLLDPNDTV
                                                                                                                                                                                                                                                Watch 50.4%; Local Similarity 42.9%;
                                                                                                                                                                                                51 INLHWLQQEPDGTI
                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN;
                                                                                                                                                                                                                                                                            560 AA;
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(REL. 14, LAST SEQUENCE UPDATE)
(REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                       (REL. 01, CREATED)
(REL. 01, LAST SEC
(REL. 31, LAST AND
                                                                                                                                                                                                                                       Conservative
                                                                                                               PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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VIRUSES; NEGATIVE-ST
                                                                                  A/FOWL PLAGUE VIRUS/ROSTOCK/34).
VIRUSES; NEGATIVE-STRAND; ORTHOMYXOVIRIDAE.
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HAZ CHAIN.
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S -> L (IN)
S -> L (IN)
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Pred. No. 7.02e-01;
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                                                                                                                        ON UPDATE)
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                                                                                                                                                                                                                                                        Length 560;
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                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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                                               THRELFALL
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Query Match
Best Local S
Matches
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RA GEYER R., DIABATE S., (SEYER H., KLENK H.-D., NIEMANN H., STIRM S.,
RL GLYCOCONJ. J. 4:17-32(1987).
C. -: FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
C. CELL RECEPTORS AND FOR INITIATING INFECTION.
C. SUBUNIT: HOMOTRIMER. EACH OF THE MONOMER IS FORMED BY TWO CHAINS
C. (141 AND HA2) LINKED BY A DISULFIDE BOND.
C. (15 PTM: CLEAVAGE OF HEMAGGLUTININ INTO TWO SUBUNITS, HA1 AND HA2,
C. (161 AND HA2) LINKED BY AND SUBUNITS, HA1 AND HA2,
C. (17 PTM: CLEAVAGE OF HEMAGGLUTININ INTO TWO SUBUNITS, HA1 AND HA2,
C. (181 AND TAKES PLACE EITHER ON SMOOTH INTERNAL MEMBRANES OR AT
C. (181 AND TAKES PLACE EITHER ON SMOOTH INTERNAL MEMBRANES OR AT
C. (181 AND TAKES PLACE EITHER ON SMOOTH INTERNAL MEMBRANES OR AT
C. (181 AND TAKES PATHOGENICITY.
C. (181 AND TAKES PATHOGENICITY.
C. (181 TRANSPORT OF THE HEMAGGLUTININ FROM THE ROUGH ENDOPLASMIC
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SIGNAL 1
CHAIN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCHUY W., WILL C., KURODA K., SCHOLTISSEK C., GARTEN W., KLENK H.-D.; EMBO J. 5:2831-2836(1986).
                                                                                                  51 INLHWLQQEPDGTI 64
                                                                                                                                                                                                            y Match 49.6%;
Local Similarity 42.9%;
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04070; HMIVF.
P03437; 1HGD.
                                                                                                                                                                                                                                                                                                                         563 AA;
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                                                                                                                                                                                                                                                                                                                 62702 MW;
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E -> G (IN MUTANT TS227).

S -> G (IN MUTANT TS1).

E -> G (IN MUTANT TS1).

D -> N (IN MUTANT TS227).

W: E543081E CRC32;
                                                                                                                                                                                                    Score 65; DB 1; Length 563;
Pred. No. 1.04e+00;
5; Mismatches 3; Indels
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CONNECTING PEPTIDE.
HA2 CHAIN.
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IN MUTANT TS227.
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